

Figure 1

SEQ ID NO:1
Size: 2164
DNA PKC-ζ,

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1 atgcccagca ggaccgaccc caagatggaa gggagcggcg gccgcgtccg cctcaaggcg
61 cattacgggg gggacatctt catcaccagc gtggacgccg ccacgacctt cgaggagctc
121 tgtgaggaag tgagagacat gtgtcgtctg caccagcagc acccgctcac cctcaagtgg
181 gtggacagcg aaggtgaccc ttgcacggtg tcctcccaga tggagctgga agaggctttc
241 cgcttgcccc gtcagtgcag ggatgaaggc ctcacatctc atgttttccc gagcaccctt
301 gagcagcctg gcctgccatg tccgggagaa gacaaatcta tctaccgccg gggagccaga
361 agatggagga agctgtaccg tgccaacggc cacctcttcc aagccaagcg ctttaacagg
421 agagcgtact gcggtcagtg cagcgagagg atatggggcc tcgcgaggga aggctacagg
481 tgcatacaact gcaaaactgct ggtccataag cgctgccacg gcctcgtccc gctgacctgc
541 aggaagcata tggattctgt catgccttcc caagagcctc cagtagacga caagaacgag
601 gacgccgacc ttccttccga ggagacagat ggaattgctt acatttcctc atcccggaa
661 catgacagca ttaaagacga ctccggaggac cttaagccag ttatcgatgg gatggatgga
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961 cagacgacaa gtcggttgtt cctggtcatt gactacgtca acggcgggga cctgatgttc
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1081 tgcatacggc tcaacttctt gcacgagagg gggatcatct acagggacct gaagctggac
1141 aacgtcctcc tggatgcgga cgggcacatc aagctcacag actacggcat gtgcaaggaa
1201 ggcttgggcc ctggtgacac aacgagcact ttctgcggaa ccccgaaat catcgcccc
1261 gaaatcctgc ggggagagga gtacgggttc agcgtggact ggtgggcgtt gggagtcctc
1321 atgtttgaga tgatggccgg gcgctccccg ttcgacatca tcaccgacaa cccggacatg
1381 aacacagagg actacctttt ccaagtgtat ctggagaagc ccatccggat ccccggttc
1441 ctgtcgtca aagcctccca tgttttaaaa ggatttttaa ataaggacct caaagagagg
1501 ctccgctgcc ggccacagac tggattttct gacatcaagt cccacgcgtt cttccgcagc
1561 atagactggg acttgctgga gaagaagcag gcgctccctc cattccagcc acagatcaca
1621 gacgactacg gtctggacaa ctttgacaca cagttacca gcgagccgt gcagctgacc
1681 ccagacgatg aggatgccat aaagaggatc gaccagtcag agttcgaagg ctttgagtat
1741 atcaacccat tattgctgtc caccgaggag tcggtgtgag gccgcgtgcg tctctgtcgt
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2101 tgctccgcca ggaaagttag cgtgtagcgt cctgaggaat aaaatgttcc gatgaaaaaa
2161 aaaa

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SEQ ID NO:2
Size: 592
PRT PKC-ζ

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1 MPSRTDPKME GSGGRVRLKA HYGGDIFITS VDAATTFEEL CEEVRDMCRL HQQHPLTLKW
61 VDSEGDPTCV SSQMELEEF RLRQCRDEG LIHVFPTST EQGPLPCPGE DKSIIYRRGAR
121 RWRKLYRANG HLFQAKRFNR RAYCGQCSE IWGLARQGYR CINCKLLVHK RCHGLVPLTC
181 RKHMDSVMPQ QEPVDDKNE DADLPSEETD GIAYISSSRK HDSIKDDSED LKPVIDGMDG
241 IKISQGLGLQ DFDLIRVIGR GTYAKVLLVR LKKNDQIYAM KVVKKELVHD DEDIDWVQTE
301 KHVFEQASSN PFLVGLHSCF QTTSRLFLVI EYVNGGDLMF HMQRQRKLPE EHARFYAAEI
361 CIALNFLHER GIIYRDLKLD NVLLDADGHI KLTIDYGMCKE GLPGDITST FCGTPNYIAP
421 EILRGEYGF SVDWWALGVL MFEMMAGRSP FDIITDNPDM NTEDYLFQVI LEKPIRIPRF
481 LSVKASHVLK GFLNKDPKER LGCRPQTGFS DIKSHAFRFS IDWDLLEKKQ ALPPFQPQIT
541 DDYGLDNFDT QFTSEPVQLT PDDEDAIKRI DQSEFEGFEY INPLLLSTEE SV

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Figure 2
Page 1 of 2

SEQ ID NO: 3
Size: 3663
DNA PLC-β1

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1  cagatggccg gggctcaacc cggagtgcac gccttgcaac tcaagcccg gtgctgtctc
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121 ccaattatth tgaggactga cctcagggg ttttctttt actggacaga tcaaaacaag
181 gagacagagc tactggatct cagccttgct aaagatgcca gatgtgggag acacgccaaa
241 gctcccaagg accccaaatt acgtgaactt ttggatgtgg ggaacatcgg gcgcctggag
301 cagcgcatga tcacagtggg gtatgggcct gacctcgtga acatctccca tttgaatctc
361 gtggcttttc aagaagaagt ggccaaggaa tggacaaatg aggttttcag tttggcaaca
421 aacctgctgg cccaaaacat gtccagggat gcatttctgg aaaaagccta tactaaactt
481 aagctgcaag tcaactccaga agggcggtatt cctctcaaaa acatatatcg cttgttttca
541 gcagatcgga agcgagtga aactgcttta gaggtctgta gtcttccatc ttcaaggaat
601 gattcaatac ctcaagaaga ttctactcca gaagtgtaca gagttttcct caacaacctt
661 tgccctcgac ctgaaattga taacatcttt tcagaatttg gtgcaaaaag caaaccatat
721 cttaccgttg atcagatgat ggattttatc aaccttaagc agcgagatcc tgggcttaat
781 gaaatacttt atccacctct aaaacaagag caagtccaag tatggattga gaagtatgaa
841 ccaacaaca gcctcgccag aaaaggacaa atatcagtgg atgggttcct gcgctatctg
901 agtggagaag aaaacggagt cgtttcacct gagaaactgg atttgaatga agacatgtct
961 cagccccctt ctactatth cattaattcc tcgcacaaca cctacctcac agctggccaa
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1081 gtggagctgg actgctggaa gggacggact gcagaagagg aacctgtcat caccatggc
1141 ttcaccatga caactgaaat atctttcaag gaagtgatag aagcaattgc ggagtgtgca
1201 ttaagactt caccttttcc aattctcctt tcgtttgaga accatgtgga ttcccaaaag
1261 cagcaagcca agatggcgga gtactgccga ctgatctttg gggatgccct tctcatggag
1321 cccctggaaa aatatccact ggaatctgga gttcctcttc caagccctat ggatttaatg
1381 tataaaatth tggtgaaaaa taagaagaaa tcacacaagt catcagaagg aagcggcaaa
1441 aagaagctct cagaacaagc ctccaacacc tacagtgact cctccagcat gttcgagccc
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3001 gaaatgaccc aaaagttaat agacttgaag gacaaacaac agcagcagct gcttaatctt
3061 cggcaagaac agtattatag tgaaaaatc cagaagcgag aacatattaa actgcttatt
3121 caaaagttga cggatgtcgc agaagagtgt cagaacaatc agttaagaa gctcaaaagaa
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Figure 2
Page 2 of 2

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3181 atctgtgaga aagaaaagaa agaattaaag aagaaaatgg ataaaaagag gcaggagaag
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3301 cggtcataata tccaggaagt ggtgcagtat atcaagaggc tagaagaagc gcaaagtaaa
3361 cggcaagaaa aactcgtaga gaaacacaag gaaatacgtc agcagatcct ggatgaaaag
3421 cccaagctgc aggtggagct ggagcaagaa taccaagaca aattcaaaaag actgcccctc
3481 gagatttttg aattcgtgca ggaagccatg aaaggaaaga tcagtgaaga cagcaatcac
3541 ggttctgccc ctctctccct gtcctcagac cctggaaaag tgaaccacaa gactccctcc
3601 agtgaggagc tgggaggaga catcccagga aaagaatttg atactcctct gtgaatgctc
3661 ctg
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SEQ ID NO:4
Size: 1216
PRT PLC-β1

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1  MAGAQPGVHA LQLKPVCVSD SLKKGTKFVK WDDSTIVTP IILRTDPQGF FFYWTDQNK
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121 AFQEEVAKAW TNEVFSLATN LLAQNMSRDA FLEKAYTKLK LQVTPGGRIP LKNIYRLFSA
181 DRKRVETALE ACSLPSSRND SIPQEDFTPE VYRVFLNNLC PRPEIDNIFS EFGAKSKPYL
241 TVDQMMDFIN LKQRDPRLNE ILYPPLKQEQ VQVLEIKYEP NNSLARKGQI SVDGFMRYLS
301 GEENGVSPE KLDLNEDEMSQ PLSHYFINSS HNTYLTAGQL AGNSSVEMYR QVLLSGCRCV
361 ELDCWKGRTA EEPVITHGF TMTTEISFKE VIEAIAECAP KTSPPFILLS FENHVDSPPKQ
421 QAKMAEYCRL IFGDALLMEP LEKYPLESGV PLPSPMDLMY KILVKNKKKS HKSSESGGKK
481 KLSEQASNTY SDSSSMFEPs SPGAGEADTE SDDDDDDDDDC KKSSMDEGTA GSEAMATEEM
541 SNLVNYIQPV KFESFEISK RNKSFEMSSF VETKGLEQLT KSPVEFVEYN KMQLSRIYPK
601 GTRVDSSNYM PQLFWNAGCQ MVALNFQTM LAMQINMGMY EYNGKSGYRL KPEFMRRPDK
661 HFDPFTEGIV DGIVANTLSV KIISGQFLSD KKVGTVEVD MFGLPVDTRR KAFKTKTSQG
721 NAVNPWEEE PIVFKKVLP TLACLRIVY EEGGKFIGHR ILPVQAIRPG YHYICLRNER
781 NQPLTLPAVF VYIEVKDYVP DTYADVIEAL SNPIRYVNLN EQRAKQLAAL TLEDEEEVKK
841 EADPGETPSE APSEARTTPA ENGVNHTTTL TPKPPSQALH SQPAPGSVKA PAKTEDLIQS
901 VLTEVEAQTI EELKQKSFV KLQKKHYKEM KDLVKRHHKK TTDLIKEHTT KYNEIQNDYL
961 RRRRAALEKSA KKDSKKKSEP SSPDHGSSTI EQDLAALDAE MTQKLIDLKD KQQQQLNLN
1021 QEQQYSEKYQ KREHIKLLIQ KLTDAEECQ NNQLKKLKEI CEKEKKELKK KMDKKRQEKI
1081 TEAKSKDKSQ MEEKTE MIR SYIQEVVQYI KRLEEAQSKR QEKLVEKHKE IRQQILDEKP
1141 KLQVELEQY QDKFKRLPLE ILEFVQEAMK GKISED SNHG SAPLSLSSDP GKVNHKTPSS
1201 EELGGDIPGK EFDTP
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Figure 3
Page 1 of 2

SEQ ID NO:5
Size: 3052
DNA FAK

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1 ccggtgtgaa ggccatgagt gattactggg ttgttggaaa gaagtctaac tatgaagtat
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121 ccaaaacact aagaaaactg atccaacaaa cathtagaca atttgccaac cttaatagag
181 aagaaagtat tctgaaattc tttgagatcc tgtctccagt ctacagattt gataaggaat
241 gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcggcccag
301 aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca
361 ctcaagtgca aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac
421 aactaaaaat agcagggtgca cccgagcctc tgacagtgac ggcaccatcc ctaaccattg
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601 ccaacagcga aaagcaaggc atgcgacac acgccgtctc tgtgtcagaa acagatgatt
661 atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga
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2881 gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg
2941 aagaacaatt tatgttcaca ttaagatagc ttctaaaggg ggttgccaa ggggtgacat
3001 cttaattcct aaactacctt agctgcatag tggaaaggga gagccggaat tc
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Figure 3
Page 2 of 2

SEQ ID NO:6
Size: 879
PRT FAK

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1  MSDYWVVGKK SNYEVLKDV GLKRFFPKSL LDSVKAKTLR KLIQQTFRQF ANLNREESIL
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121 IQYSNSEDKD RKGMLQLKIA GAPEPLTVTA PSLTIAENMA DLIDGYCRLV NGTSQSFIIR
181 PQKEGERALP SIPKLANSEK QGMRTHAVSV SETDDYAEII DEEDTYTMPs TRDYEIQRER
241 IELGRCIGEG QFGDVHQGIY MSPENPALAV AIKTCKNCTS DSVREKFLQE ACHYTSLHWN
301 WCRYISDPNV DACPDPRNAE LTMRFQDHPH IVKLIGVITE NPVWIIMELC TLGELRSFLQ
361 VRKYSLDLAS LILYAYQLST ALAYLESKRF VHRDIAARNV LVSSNDCVKL GDFGLSRYME
421 DSTYYKASKG KLPIKWMAPE SINFRRFTSA SDVWMFGVCM WEILMHGVKP FQGVKNNDVI
481 GRIENGERLP MPPNCPPTLY SLMTKCWAYD PSRRPRFTEL KAQLSTILEE EKAQQEERM
541 MESRRQATVS WDSGGSDEAP PKPSRPGYPS PRSSEGFYPS PQHMQVTNHY QVSGYPGSHG
601 ITAMAGSIYP GQASLLDQTD SWNHRSQEIA MWQPNVEDST VLDLRGIGQV LPTHLMEERL
661 IRQQQEMEED QRWLEKEERF LIGNQHIYQP VGKPDPAAPP KKPPRPGAPG HLGSLASLSS
721 PADSYNBVGK LQPQEISPPP TANLDRSNDK VYENVTGLVK AVIEMSSKIQ PAPPEEYVPM
781 VKEVGLALRT LLATVDETIP LLPASTHREI EMAQKLLNSD LGELINKMKL AQQYVMTSLQ
841 QEYKKQMLTA AHALAVIDAKN LLDVIDQARL KMLGQTRPH
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Figure 4
Page 1 of 2

SEQ ID NO:7
Size: 4089
DNA FAK2

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61 cggccgactt acctgtactt gccgccgtcc cggctcacct ggcggtgccc gaggagtagt
121 cgctggagtc cgcgcctccc tgggactgca atgtgccgat cttagctgct gcctgagagg
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1621 ctgcaccacc cgcacatcgt gaagctgatc ggcatcattg aagaggagcc cacctggatc
1681 atcatggaat tgtatcccta tggggagctg ggccactacc tggagcggaa caagaactcc
1741 ctgaagggtc tcacctcgt gctgtactca ctgcagatat gcaaagccat ggcctaccgt
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1861 gagtgtgtga agctggggga ctttggctct tcccggtaca ttgaggacga ggactattac
1921 aaagcctctg tgactcgtct ccccatcaaa tggatgtccc cagagtccat taacttccga
1981 cgcttcacga cagccagtga cgtctggatg ttccgctgtg gcatgtggga gatcctgagc
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2161 tgctgggact acgacccagc tgaccggccc cgcttcaccg agctgggtgtg cagcctcagt
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2281 acccccaaaa tcttggagcc cacagccttc caggaacccc caccgaagcc cagccgacct
2341 aagtacagac cccctccgca aaccaacctc ctggctccaa agctgcagtt ccaggttcct
2401 gaggggtctg gtgccagctc tctacgctc accagcccta tggagtatcc atctcccgtt
2461 aactcactgc acacccacc tctccaccgg cacaatgtct tcaaacgcca cagcatgggg
2521 gaggaggact tcatccaacc cagcagccga gaagaggccc agcagctgtg ggaggctgaa
2581 aagggtcaaaa tgcggcaaat cctggacaaa cagcagaagc agatggtgga ggactaccag
2641 tggctcaggg aggaggagaa gtccttgagc cccatggttt atatgaatga taagtcccca
2701 ttgacgcagc agaaggaggt cggctacctg gatttcacag ggcacccaca gaagcccccg
2761 aggtcgggag cacagtccat ccagccacac gctaacctgg accggaccga tgacctggtg
2821 tacctcaatg tcatggagct ggtgcggggc gtgctggagc tcaagaatga gctctgtcag
2881 ctgccccccg agggctacgt ggtggtggtg aagaatgtgg ggctgacctt gcggaagctc
2941 atcgggagcg tggatgatct cctgccttcc ttgcccgtcat cttcacggac agagatcgag
3001 ggcacccaga aactgctcaa caaagacctg gcagagctca tcaacaagat gcggctggcg
3061 cagcagaacg ccgtgacctc cctgagtgag gagtgaaga ggcagatgct gacggcttca
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3181 gccaatctgg cccaccacc tgcagagtga cggagggtgg gggccacctg cctgcgtctt
3241 ccgcccctgc ctgccatgta cctcccctgc cttgctgttg gtcagtgtgg tcttccaggg
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Figure 4
Page 2 of 2

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3301 agaaggccaa ggggagtcac cttcccttgc cactttgcac gacgccctct cccacccct
3361 acccctggct gtactgctca ggctgcagct ggacagaggg gactctgggc tatggacaca
3421 ggggtgacggg gacaaagatg gctcagaggg ggactgctgc tgccctggcca ctgctcccta
3481 agccagcctg gtccatgcag ggggctcctg ggggtgggga ggtgtcacat ggtgcccta
3541 gctttatata tggacatggc aggccgattt gggaaaccaag ctattccttt ccttcctct
3601 tctccctca gatgtccctt gatgcacaga gaagctgggg aggagctttg ttttcggggg
3661 tcaggcagcc agtgagatga gggatgggcc tggcattctt gtacagtgtg tattgaaatt
3721 tatttaatgt gaggtttggt ctggactgac agcatgtgcc ctcctgaggg aggaccaggg
3781 cacagtccag gaacaagcta attgggagtc caggcacagg atgctgtgtt gtcaacaaac
3841 caagcatcag ggggaagaag cagagagatg cggccaagat aggaccttg gccaaatccg
3901 ctctcttctt gcccctcttt ctctttcttc ctttactttt ccttgctttt cctctttttc
3961 ttactcctcc tctttctctc cccaccccc attctcatct gcaccttct tttctcatgt
4021 gtttgcataa acattctttt aacttctttc tatttgactt gtggttgaat taaaattgtc
4081 ccatttgca
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SEQ ID NO:8
Size: 1009
PRT FAK2

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1 MSGVSEPLSR VKLGTLLRPE GPAEPMVVVP VDVEKEDVRI LKVCFYNSNF NPGKNFKLVK
61 CTVQTEIREI ITSILLSGRI GPNIRLAECY GLRLKHKMSD EIHWHLPQMT VGEVQDKYEC
121 LHVEAEWRYD LQIRYLPEDF MESLKEDRTT LLYFYQQLRN DYMORYASKV SEGMAQLGQC
181 LELRRFFKDM PHNALDKKSN FELLEKEVGL DLFFPKQMQE NLKPKQFRKM IQQTFQQYAS
241 LREEECVMKF FNTLAGFANI DQETYRCELI QGWNITVDLV IGPKGIRQLT SQDAKPTCLA
301 EFKQIRSIRC LPLEEGQAVL QLGIEGAPQA LSIKTSSLAE AENMADLIDG YCRLQGEHQG
361 SLIIHPRKDG EKRNSLPQIP MLNLEARRSH LSESCSIESD IYAEIPDETL RRPGGPQYGI
421 AREDVVLNRI LGEGFFGEVY EGVYTNHKG E KINVAVKTC KDCTLDNKEK FMSEAVIMKN
481 LDHPHIVKLI GIIEEPTWI IMELYPYGEL GHYLERNKNS LKVLTLVLVS LQICKAMAYL
541 ESINCVHRDI AVRNLVASP ECVKLGDFGL SRYIEDEDY KASVTRLPIK WMSPEINFR
601 RFTTASDVWM FAVCMWEILS FGKQPFVLE NKDVIGVLEK GDRLPKPDLC PPVLYTLMTR
661 CWDYDPSDRP RFTELVCSLD DVYQMEKDIA MEQERNARYR TPKILEPTAF QEPKPKPSRP
721 KYRPPQTNL LAPKLQFQVP EGLCASSPTL TSPMEYPSPV NSLHTPPLHR HNVFKRHSR
781 EEDFIQSSR EEAQQLWEAE KVKMRQILDK QKQMVVEDYQ WLRQEEKSLD PMVYMNDKSP
841 LTPEKEVGYL EFTGPPQKPP RLGAQSIQPT ANLDRDLDLV YLNMELVRA VLELKNELCQ
901 LPPEGYVVVV KNVGLTLRKL IGSVDDLLPS LPSSSRTEIE GTQKLLNKDL AELINKMRLA
961 QQNAVTSLS ECKRQMLTAS HTLAVDAKNL LDAVDQAKVL ANLAHPPAE
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Figure 5

SEQ ID NO:9
Size: 2195
DNA CK2

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1 aggggagagc ggccgcccgc gctgccgctt ccaccacagt ttgaagaaaa caggtctgaa
61 acaaggtctt acccccagct gcttctgaac acagtgactg ccagatctcc aaacatcaag
121 tccagctttg tccgccaacc tgtctgacat gtcgggaccc gtgccaagca gggccagagt
181 ttacacagat gttaatacac acagacctcg agaatactgg gattacgagt cacatgtggt
241 ggaatgggga aatcaagatg actaccagct ggttcgaaaa ttaggccgag gtaaatacag
301 tgaagtattt gaagccatca acatcacaaa taatgaaaaa gttgtgttta aaattctcaa
361 gccagtaaaa aagaagaaaa ttaagcgtga aataaagatt ttggagaatt tgagaggagg
421 tcccaacatc atcacactgg cagacattgt aaaagaccct gtgtcacgaa cccccgcctt
481 ggtttttgaa cacgtaaaca acacagactt caagcaattg taccagacgt taacagacta
541 tgatattcga ttttacatgt atgagattct gaaggccctg gattattgtc acagcatggg
601 aattatgcac agagatgtca agccccataa tgtcatgatt gatcatgagc acagaaagct
661 acgactaata gactgggggt tggctgagtt ttatcatcct ggccaagaat ataatgtccg
721 agttgcttcc cgatacttca aaggctcctga gctacttgta gactatcaga tgtacgatta
781 tagtttggtt atgtggagtt tgggtgtgat gctggcaagt atgatcttcc ggaaggagcc
841 atttttccat ggacatgaca attatgatca gttggtgagg atagccaagg ttctggggac
901 agaagattta tatgactata ttgacaaata caacattgaa ttatgatccac gtttcaatga
961 tatcttgggc agacactctc gaaagcgatg ggaacgcttt gtccacagtg aaaatcagca
1021 ccttgtcagc cctgaggcct tggatttcct ggacaaaactg ctgcatatg accaccagtc
1081 acggcttact gcaagagagg caatggagca cccctatttc tacactgttg tgaaggacca
1141 ggctcgaatg ggttcacta gcatgccagg gggcagtagc cccgtcagca gcgccaatat
1201 gatgtcaggg atttcttcag tgccaacccc ttcacccctt ggacctctgg caggctcacc
1261 agtgattgct gctgccaacc ccttgggat gcctgttcca gctgccgctg gcgctcagca
1321 gtaacggccc tatctgtctc ctgatgcctg agcagagggtg ggggagtgca cctctcctt
1381 gatgcagctt gcgcctggcg gggaggggtg aaacacttca gaagcaccgt gtctgaaccg
1441 ttgcttgtgg atttatagta gttcagtcac aaaaaaaaaa ttataatagg ctgattttct
1501 tttttctttt tttttttaac tcgaactttt cataactcag gggattccct gaaaaattac
1561 ctgcaggtgg aatatttcat ggacaaaatt ttttttctcc cctcccaaat ttagttcctc
1621 atcacaaaaa aacaaaagata aaccagcctc aatcccggct gctgcattta ggtggagact
1681 tcttccattt cccaccattg ttctccacc gtcccacact ttagggggtt ggtatctcgt
1741 gctcttctcc agagattaca aaaatgtagc ttctcagggg aggcaggaag aaaggaagga
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1861 catcacttta ctccataagc gcttcagtg ggttatccta gtggctcttg tggagtggtg
1921 tcttagttac atcaagatgt tgaaaatcta cccaaaatgc agacagatac taaaaacttc
1981 tggttcagtaa gaatcatgtc ttactgatct aaccctaaat ccaactcatt tatactttta
2041 tttttagttc agtttaaaat gttgatacct tccctcccag gctccttacc ttggtctttt
2101 cctgttcat ctccaacat gctgtgctcc atagctggta ggagagggaa ggcaaaatct
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SEQ ID NO:10
Size: 391
PRT CK2

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1 MSGPVPSRAR VYTDVNTHRP REYWDYESHV VEWGNQDDYQ LVRKLGRGKY SEVFRAINIT
61 NNEKVVVKIL KPVKKKKIKR EIKILENLRG GPNIITLADI VKDPVSRTPA LVFEHVNNTD
121 FKQLYQTLTD YDIRFYMYEI LKALDYCHSM GIMHRDVKPH NVMIDHEHRK LRLIDWGLAE
181 FYHPGQEYNV RVASRYFKGP ELLVDYQMYD YSLDMWSLGC MLASMI FRKE PFFHGHNDNYD
241 QLVRIAKVLG TEDLYDYIDK YNIELDPRFN DILGRHSRKR WERFVHSENQ HLVSPÉALDF
301 LDKLLRYDHQ SRLTAREAME HPYFYTVVKD QARMGSSSMP GGSTPVSSAN MMSGISSVPT
361 PSPLGPLAGS PVIAAANPLG MPVPAAGAGQ Q

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Figure 6
Page 1 of 2

SEQ ID NO: 11
Size: 4626
DNA cMET

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1  gaattccgcc  ctgcgcgcgc  ggggcgcgcc  gaggcgctttg  tgagcagatg  cggagccgag
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121  cggagcgcgc  gtgtggtcct  tgcgcgcgtg  acttctccac  tggttcctgg  gcaccgaaag
181  ataaacctct  cataatgaag  gccccgcgtg  tgcttgacc  tggcatctc  gtgctcctgt
241  ttaccttggt  gcagaggagc  aatggggagt  gtaaagaggc  actagcaaag  tccgagatga
301  atgtgaatat  gaagtatcag  cttcccaact  tcaccgcgga  aacacccatc  cagaatgtca
361  ttctacatga  gcatcacatt  ttcttgggtg  ccactaacta  catttatgtt  ttaaattgag
421  aagaccttca  gaaggttgct  gagtacaaga  ctgggcctgt  gctggaacac  ccagattgtt
481  tcccatgtca  ggactgcagc  agcaaagcca  atttatcagg  aggtgtttgg  aaagataaca
541  tcaacatggc  tctagtgtgc  gacacctact  atgatgatca  actcattagc  tgtggcagcg
601  tcaacagagg  gacctgccag  cgacatgtct  ttccccacaa  tcatactgct  gacatacagt
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961  acaattttat  ttacttcttg  acggtccaaa  gggaaactct  agatgctcag  acttttcaca
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1141  tacttcaggc  tgcgtatgtc  agcaagcctg  gggcccagct  tgctagacaa  ataggagcca
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1261  caatggatcg  atctgccatg  tgtgcattcc  ctatcaaata  tgtcaacgac  ttcttcaaca
1321  agatcgtcaa  caaaaacaat  gtgagatgtc  tccagcattt  ttacggacc  aatcatgagc
1381  actgctttaa  taggacactt  ctgagaaatt  catcaggctg  tgaagcgcgc  cgtgatgaat
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1561  ggacatcaga  gggtcgcttc  atgcagggtg  tggtttctcg  atcaggacca  tcaaccctc
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2521  gcacaataac  aggtgttggg  aaaaacctga  attcagttag  tgtcccgaga  atggtcataa
2581  atgtgcatga  agcaggaagg  aactttacag  tggcatgtca  acatcgctct  aattcagaga
2641  taatctgttg  taccactcct  tccctgcaac  agctgaatct  gcaactcccc  ctgaaaacca
2701  aagccttttt  catgttagat  gggatccttt  ccaaatactt  tgatctcatt  tatgtacata
2761  atcctgtgtt  taagcctttt  gaaaagccag  tgatgatctc  aatgggcaat  gaaaatgtac
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2881  gaaataagag  ctgtgagaat  atacacttac  attctgaagc  cgttttatgc  acggtcccca
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3001  ccgtccttgg  aaaagtaata  gttcaaccag  atcagaattt  cacaggattg  attgctgggtg
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3121  gaaagcaaat  taaagatctg  ggcagtgaat  tagttcgcta  cgatgcaaga  gtacacactc
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Figure 6
Page 2 of 2

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3241 atgaatctgt agactaccga gctacttttc cagaagatca gtttcctaata tcatctcaga
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3781 taaaagatct tattggcttt ggtcttcaag tagccaaagc gatgaaatat cttgcaagca
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3961 acaacaaaac aggtgcaaag ctgccagtga agtggatggc tttggaaagt ctgcaaactc
4021 aaaagtttac caccaagtca gatgtgtggt cctttggcgt cgtcctctgg gagctgatga
4081 caagaggagc cccaccttat cctgacgtaa acacctttga tataactgtt tacttgttgc
4141 aagggagaag actcctacaa cccgaatact gcccagacc cttatatgaa gtaatgctaa
4201 aatgctggca ccctaaagcc gaaatgcgcc catccttttc tgaactgtg tcccggatat
4261 cagcgatctt ctctactttc attggggagc actatgtcca tgtgaacgct acttatgtga
4321 acgtaaaatg tgtcgctccg tatecttctc tgttgtcatc agaagataac gctgatgatg
4381 aggtggacac acgaccagcc tcttctgagg agacatcata gtgctagtac tatgtcaaag
4441 caacagtcca cactttgtcc aatgggtttt tctactgcctg accttataaa ggccatcgat
4501 attctttgct ccttgccata ggacttgtat tgttatttaa attactggat tctaaggaat
4561 ttcttatctg acagagcatc agaaccagag gcttggtccc acaggccagg gaccaatgcg
4621 ctgcag
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SEQ ID NO:12
Size: 1408
PRT cMET

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1 MKAPAVLAPG ILVLLFTLVQ RSNGECKEAL AKSEMNVNMK YQLPNFTAET PIQNVILHEH
61 HIFLGATNYI YVLNEEDLQK VAEYKTGPVL EHPDCFPQCD C$SKANLSSG VWKDNINMAL
121 VVDITYDDQL ISCGSVNRGT CORHVFPHNH TADIQSEVHC IFSPQIEEPS QCPDCVVSAL
181 GAKVLSSVKD RFINFFVGNT INSSYFPDHP LHSISVRLK ETKDGFMLT DQSYIDVLPE
241 FRDSYPIKYV HAFESNNFIY FLTVQRETLA AQTFHTRIIR FCSINSLHS YMEMPLECIL
301 TEKRKKRSTK KEVFNILQAA YVSKPGAQLA RQIGASLNDD ILFGVFAQSK PDSAEPMDRS
361 AMCAFPKIVY NDFFNKIVNK NNVRCLQHFY GPNHEHCFNR TLLRNSSGCE ARRDEYRTEF
421 TTALQRVDLF MGQFSEVLLT SISTFIKGD L TIANLGTSEG RFMQVVVSRS GPSTPHVNFL
481 LD$HPVSPEV IVEHTLNQNG YTLVITGKKI TKIPLNGLGC RHFQSCSQCL SAPPFVQCGW
541 CHDKCVRSEE CLSGTWTQOI CLPAIYKVFP NSAPLEGGTR LTICGWDFGF RRNNKFDLKK
601 TRVLLGNESC TLTLSESTMN TLKCTVGPAM NKHFNM$III SNGHGTQYS TFSYVDPVIT
661 SISPKYGPM$ GGTLLTLTGN YLNSGNSRHI SIGGKTCTLK SVSNSILECY TPAQTISTEF
721 AVKLKIDLAN RETSIFSIRE DPIVYEIHPT KSFISTWWKE PLNIVSFLFC FASGGSTITG
781 VGKNLNSVSV PRMVINVHEA GRNFTVACQH RSNSEIICCT TPSLQQLNLQ LPLKTKAFFM
841 LDGILSKYFD LIYVHNPFVK PFEKPMISM GNENVLEIKG NDIDPEAVKG EVLKVGNKSC
901 ENIHLHSEAV LCTVPNDLLK LNSELNIEWK QAI$STVLGK VIVQPDQNF GLIAGVVSIS
961 TALLLLLGFF LWLKKRKQIK DLGSELVRYD ARVHTPHLDR LVSARSVSPT TEMVSNESVD
1021 YRATFPEDQF PNSSQNGSCR QVQYPLTDM$ PILTSGDS DI SSPLLQNTVH IDLSALNP EL
1081 VQAVQHVVIG PSSLIVHFNE VIGRGHFGCV YHGTL$NDNG KKIHC$VKS L NRITDIGEVS
1141 QFLTEGIIMK DFSHPNVLSL LGICLRSEGS PLVVL$PYMKH GD$RNFIRNE THNP$VKDLI
1201 GFGLQVAKAM KYLASKKFVH RDLAARNCML DEKFTVKVAD FGLARDMYDK EYYSVHNKTG
1261 AKLPVKWMAL ESLQTQKFTT KSDVWSFGVV LWELMTRGAP PYPDVNTFDI TVYLLQGRRL
1321 LQPEYCPDPL YEVM$K$WHP KAEMRPSFSE LVSRI$AIFS TFIGEHYVHV NATYVNVKCV
1381 APYPSLLSSE DNADDEV$TR PASFWETS
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Figure 7
Page 1 of 2

SEQ ID NO:13
Size: 3350
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1  cacagtccac tctgtcaggg tttaaggcag gaaaaacatg ctcatTTtga tggtaatat
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121 aataaatTTg aatgaaatca aggatgaagt ccttgggatg acttgTtctc tcatccttga
181 aacagttcag aagactatgg acaaagatta tttcaaccag actctgaatg tcctaaatac
241 aactacaaac cacaaatatg ccttggcatt ggccTTtaca gtggatgaaa tcaacaggaa
301 tcctgatctt ttaccaaata tgtctctgat tataaaatac aatttgggtc atttgtatgg
361 aaaaactgta acaactctat ccgatttatt taatccaaat aatcatctcc atttcccaa
421 ttatttatgt aatgaaggga ttatgtgttt ggttctgctt acaggaccac attggagagc
481 atctttatat ctctggatat ccgtgtatgt ctacctgtct ccacatttcc ttcagctttc
541 ctatggacct ttctactcca tcttcagtga taatgaacaa tatccttate tctatcagat
601 gggcccaaag gactcatcac tagcattggc aatggTctcc ttcataatTT acttcaagtG
661 gaactgggtt gggctatttt tctcagatga tgatcaaggc aatcaatttc tctcagagtt
721 gaaaaaagag agccaaacca aggatatttg ctttgccttt gtgaacatga tatcagtcag
781 tgatgtttca tactatcata aaactgaaat gtactacaac caaattgtga tgtcatccac
841 aaaggttatt atcatttatg gggaaacaaa cagtattatt gaattgagct tcagaatgtg
901 gtcactctca gttaaacaga gaatatgggt caccacaaaa caatttgatt gccctaccag
961 taagagagac ttaactcatg gcacattcta tgggaccctt acatttctac accactatgg
1021 tgagatttct ggctttaaaa attttgtaca gacacggtac aatctcagaa gcacagattt
1081 atatctagta atgccagagt ggaaatattt taactatgaa gcctcagcat ctaactgtaa
1141 aatactgaga aactattttat ccaatatctc actggaatgg ctaatggaac agaaatttga
1201 catgtcattt agtgattata gtcacaacat atacaatgct gtatatgcca ttgctcatgc
1261 actccatgag aagaatctgc aagaagtTga aaatcaggca ataaacaatg cgaaaggaga
1321 aaatactcac tgcttgaagc taaactcatt tctgagaaag acccacttca ctaattctct
1381 tgggaacaga gtaattatga aacagagaga agtagtgcat ggagactata atattgttca
1441 catgttgaat ttctcacaac gccttgggat taaggTgaag ataggacaat tcagcccaca
1501 ttttccacag ggtcaacagt tacacttata tgtagacatg actgagttgg ctacaggaag
1561 tagaaagatg ccatcctcag tgtgcagtgc agattgccat cctggattca gaagaatctg
1621 gaaggaggaa atggcagcct gctgttttgt ttgcaacccc tgccctgaaa atgaaatttc
1681 taatgagacg atgggtggtat tttgggtctt cgtgaagcac catgacactc ctattgtgaa
1741 ggccaataac agaatcctca gctacctatt aatcgtgtca ctcatgttct gttttctgtg
1801 ctccTTTTtTc ttcatTggct atcctaacag agcaacctgt atcttacagc aaatcacatt
1861 tggaaTcttTc tttactgtgg ctatttccac agttctggcc aaaacaatca ctgtggttct
1921 ggctttTcaaa gtcacagacc caggaaagac attaagaatc tttttggTat cggggacacc
1981 caactacatt attcccatat gttccctatt gcaatgtatt ctgtgtgcaa tctggctagc
2041 agttttctcct ccctttgttg atattgatga acactctgag catggccaca tcatcattgt
2101 gtgcaacaag ggctccatta ctgcattcta ctgtgtcctg ggatacttgg cctgcctggc
2161 ctttTggaagc ttcactatag ctttcttggc aaagaacctg cctgacacat tcaacgaagc
2221 caagttcttg accttcagca tgctagtgtt ctgcgctgtc tgggtcacct tcctccctgt
2281 ctaccatagc accaagggca aggtcatggt tgctgtggag atcttctcca tcttggcatc
2341 tagtgcaggg atgctgggat gcactttTgc acccaaagtt tacatcattt taatgagacc
2401 agacagaaat tcgatccaca aaatcaggga gaaatcatat ttctgaaaag gtatttcagg
2461 aattctgtca aatgtaaagt tgatacatac accccaaata tttagttaca gagcatatat
2521 ctagtTTtag aatcactctc actggttctc ctagttaagc atagaagtac catatgtact
2581 gatcttTgcat atgttgtcta taaaatctta caatcattca tttgcttagt atcttctTga
2641 agaagTaaaa ttttcaaata actagtacaa ttttattcat tattttgctt tcatgaggat
2701 ttccccctgg taacttcaaa taaattttat aagtcagttg aatatataac cttacataga
2761 aagtgaagTtC taggacagac agggattata catagaaaca aactaactaa aaatcaacaa
2821 agatgaaatc agaacacatt ttcttatttc cagtaggaac acatactTga cagaatactg
2881 tctttttttc agctgctctt taagatatTg gccaatagtc taagtTaaa atgttcttta
2941 tctactctca aatacaaaaa tattatatcc aacaatggac agaactctgag aactcctgtg
3001 gttgagTtag ggaatagttg gaagatactg agaaggaggt gacctatagg aatacaaaagc
3061 agtctcaact aacctggaca accaaggTcc ctgagacact gagccactaa caagtcagcc
3121 tactccagct gttatgaggc ccccaaaaaa tatgcaacat aggattgcct ggtccagcct
```

Figure 7
Page 2 of 2

```
3181 cagcaagaga atacacacct aaccacagag agacttcccc aagggtattgg ggaggtctgg
3241 ggtttggaga gttgcggatt gtcccttgat gattggaagg aggtattgga tgagaatgaa
3301 tcaggggggaa gactaggaag gggataatga tgggaactgta aaaaaaaaaa
```

SEQ ID NO:14
Size: 380
PRT FENI

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1 MGIQGLAKLI ADVAPSAIRE NDIKSYFGRK VAIDASMSIY QFLIAVRQGG DVLQNEEGET
61 TSHLMGMFYR TIRMMENGIK PVYVFDGKPP QLKSGELAKR SERRAEAEKQ LQQAQAAGAE
121 QEVEKFTKRL VKVTKQHND CKHLLSLMGI PYLDAPSEAE ASCAALVKAG KVVAAATEDM
181 DCLTFGSPVL MRHLTASEAK KLPIQEFHLS RILQELGLNQ EQFVDLCILL GSDYCESIRG
241 IGPKRAVDLI QKHKSIEEIV RRLDPNKYPV PENWLHKEAH QLFLEPEVLD PESVELKWSE
301 PNEEELIKFM CGEKQFSEER IRSGVKRLSK SRQGSTQGRL DDFFKVTGSL SSAKRKEPEP
361 KGSTKKKAKT GAAGKFKRGK
```

Figure 8
Page 1 of 2

SEQ ID NO:15
Size: 4276
DNA REV1

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1 agagccaccg cggagcgcgc ggggggttgg ttgccgcgag cgtggggggag cgtggaccgc
61 ggcgctgctc agcgggtgggg ctgccttccc cgggccctcc tccctgggtcc ctggcgaggg
121 cactggcggc ggcggggccg ggggtccgcaa ggccggagaa ggccgcccggg cccgggcatg
181 gtggtctggg gcaacgcgga agaagctcca ccatgaggcg aggtggatgg aggaagcgag
241 ctgaaaatga tggctgggaa acatgggggtg ggtatatggc tgccaagggtc cagaaattgg
301 aggaacagtt tcgatcagat gctgctatgc agaaggatgg gacttcactc acaattttta
361 gtggagtgtc catctatgtt aatggataca cagatccttc cgctgaggaa ttgagaaaac
421 taatgatgtt gcatggagggt caataccatg tatattattc cagatctaaa acaacacata
481 ttattgccac aaatcttccc aatgccccaa ttaaagaatt aaagggggaa aaagtaattc
541 gaccagaatg gattgtggaa agcatcaaag ctggacgact cctctcctac attccatata
601 agctgtacac caagcagtcc agtgtgcaga aaggctcag ctttaactct gtatgcagac
661 ctgaggatcc tctgccagggt ccaagcaata tagccaaaca gctcaacaac agggtaaatac
721 acatcggtta gaagattgaa acggaaaatg aagtcaaagt caatggcatg aacagttgga
781 atgaagaaga tgaaaataat gatttttagtt ttgtggatct ggagcagacc tctccgggaa
841 ggaaacagaa tgggaattccg catcccagag ggagcactgc catttttaac ggacacactc
901 ctagctctaa tgggtgcctta aagacacagg attgcttggg gccctgggtc aacagtgttg
961 ccagcagggt ttctccagcc ttttcccagg agggagataa ggctgagaag agcagcactg
1021 atttcagaga ctgcactctg cagcagttgc agcaaagcac cagaaacaca gatgctttgc
1081 ggaatccaca cagaactaat tctttctcat tatcaccttt gcacagtaac actaaaatca
1141 atgggtgctc cactccact gttcaggggc cttcaagcac aaaagcact tcttcagtat
1201 ctacgtttag caaggcagca ccttcagtgc catccaaacc ttcagactgc aattttattt
1261 caaacttcta ttctcattca agactgcata acatatcaat gtggaagtgt gaattgactg
1321 agtttgtcaa taccctacaa agacaaagta atggtatctt tccaggaagg gaaaagttaa
1381 aaaaaatgaa aacaggcagg tctgcacttg ttgtaactga cacaggagat atgtcagtat
1441 tgaattctcc cagacatcag agctgtataa tgcagtgtga tatggtatgc tctttgtat
1501 cagtgggtat acgaaataga ccagatctca aaggaaaacc agtggctgtt acaagtaaca
1561 gaggcacagg aagggcacct ttacgtcctg gcgctaaccc ccagctggag tggcagtatt
1621 accagaataa aatcctgaaa ggcaaagcag cagatatacc agattcatca ttgtgggaga
1681 atccagattc tgcgcaagca aatggaattg attctgtttt gtcaagggtc gaaattgcat
1741 cttgtagtta tgaggccagg caacttggca ttaagaacgg aatgtttttt gggcatgcta
1801 aacaactatg tcctaactct caagctgttc catacgattt tcatgcatat aaggaagtgc
1861 cacaacatt gtatgaaaca ttggcaagct acactcataa cattgaagct gtcagtgtg
1921 atgaagcgct ggtagacatt accgaaatcc ttgcagagac caaacttact cctgatgaat
1981 ttgcaaatgc tgttcgtatg gaaatcaaa agcagacgaa atgtgtgccc tctgttggaa
2041 ttggttctaa tattctcctg gctagaatgg caactagaaa agcaaaaacca gatgggcagt
2101 accacctaaa accagaagaa gtagatgatt ttatcagagg ccagctagtg accaatctac
2161 caggagtgg acattcaatg gaatctaagt tggcatcttt gggaattaaa acttgtggag
2221 acttgcagta tatgaccatg gcaaaactcc aaaaagaatt tgggtcccaa acaggtcaga
2281 tgctttatag gttctgccgt ggcttggatg atagaccagt tcgaactgaa aaggaaagaa
2341 aatctgtttc agctgagatc aactatggaa taaggtttac tcagccaaaa gaggcagaag
2401 cttttcttct gagtctttca gaagaaattc aaagaagact agaagccact ggcataaggg
2461 gtaaacgtct aactctcaaa atcatggtac gaaagcctgg ggctcctgta gaaactgcaa
2521 aatttggagg ccatggaatt tgtgataaca ttgccaggac tgtaactctt gaccaggcaa
2581 cagataatgc aaaaataatt ggaaaggcga tgctaaacat gtttcataca atgaaactaa
2641 atatatcaga tatgagaggg gttgggattc acgtgaatca gttggttcca actaatctga
2701 acccttccac atgtcccagt cgcccatcag ttcagtcaag ccactttcct agtgggtcat
2761 actctgtccg tgatgtcttc caagtccaga aagctaagaa atccaccgaa gaggagcaca
2821 aagaagtatt tcgggctgct gtggatctgg aaatatcatc tgcttctaga acttgcactt
2881 tcttgccacc ttttcttgca catctgccga ccagtcctga tactaacaag gctgagtctt
2941 cagggaatg gaatggctca catactcctg tcagtgtgca gtcgagactt aacctgagta
3001 tagaggctcc gtcaccttcc cagctggatc agtctgtttt agaagcactt ccacctgatc
3061 tccgggaaca agtagagcaa gtctgtgctg tccagcaagc agagtccatc ggcgacaaaa
3121 agaaagaacc agtaaatggc tgtaatacag gaattttgcc acaaccagtt gggacagtct
3181 tgttgcaaat accagaacct caagaatcga acagtgcgc aggaataaat ttaatagccc
```

Figure 8
Page 2 of 2

```
3241 ttccagcatt ttcacaggtg gaccctgagg tatttgctgc ccttcctgct gaacttcaga
3301 gggagctgaa agcagcgtat gatcaaagac aaaggcaggg cgagaacagc actcaccagc
3361 agtcagccag cgcactctgtg ccaaagaatc ctttacttca tctaaaggca gcagtgaag
3421 aaaagaaaaa aaacaagaag aaaaaaacca ttggttcacc aaaaaggatt cagagtcctt
3481 tgaataacaa gctgcttaac agtcctgcaa aaactctgcc aggggcctgt ggcagtcccc
3541 agaagttaat tgatggggtt ctaaaacatg aaggacctcc tgcagagaaa cccctggaag
3601 aactctctgc ttctacttca ggtgtgccag gcctttctag tttgcagtct gaccagctg
3661 gctgtgtgag acctccagca cccaatctag ctggagctgt tgaattcaat gatgtgaaga
3721 ccttgctcag agaatggata actacaattt cagatccaat ggaagaagac attctccaag
3781 ttgtgaaata ctgtactgat ctaataagaag aaaaagattt ggaaaaactg gatctagtta
3841 taaaatacat gaaaaggctg atgcagcaat cgggtggaatc gggttggaat atggcatttg
3901 actttattct tgacaatgtc cagggtggtt tacaacaaac ttatggaagc acattaaaag
3961 ttacataaat attaccagag agcctgatgc tctctgatag ctgtgccata agtgcttggtg
4021 aggtatttgc aaagtgcagt atagtaatgc tcggagtttt tataatttta aatttctttt
4081 aaagcaagtg ttttgtacat ttcttttcaa aaagtgccaa atttgtcagt attgcatgta
4141 aataattgtg ttaattattt tactgtagca tagattctat ttacaaaatg tttgtttata
4201 aagttttatg gattttttaca gtgaagtgtt tacagttgtt taataaagaa ctgtatgtaa
4261 aaaaaaaaaa aaaaaa
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SEQ ID NO:16
Size: 1251
PRT REV1

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1 MRRGGWRKRA ENDGWETWGG YMAAKVQKLE EQFRSDAAMQ KDGTSSSTIFS GVAIYVNGYT
61 DPSAEELRKL MMLHGGQYHV YYSRSKTTHI IATNLPNAKI KELKGEKVIR PEWIVESIKA
121 GRLLSYIPYQ LYTKQSSVQK GLSFNPVCRP EDPLPGPSNI AKQLNNRVNH IVKKIETENE
181 VKVNGMNSWN EEDENNDFSF VDLEQTSPGR KQNGIPHPRG STAIFNGHTP SSNGALKTQD
241 CLVPMVNSVA SRLSPAFSQE EDKAEKSSTD FRDCTLQQLQ QSTRNTDALR NPHRTNSFSL
301 SPLHSNTKIN GAHHSTVQGP SSTKSTSSVS TFSKAAPSV SKPSDCNFIS NFYSHSRLHH
361 ISMWKCELTE FVNTLQRQSN GIFPGREKLK KMKTGRSALV VTDTGDMSVL NSPRHQSCIM
421 HVDMDCCFFVS VGIRNRPDLK GKPVAVTSNR GTGRAPLRPG ANPQLEWQYY QNKILKGKAA
481 DIPDSSLWEN PDSAQANGID SVLSRAEIAS CSYEARQLGI KNGMFFGHAK QLCPNLQAVP
541 YDFHAYKEVA QTLYETLAS THNIEAVSCD EALVDITEIL AETKLTPDEF ANAVRMEIKD
601 QTKCAASVGI GSNILLARMA TRKAKPDGQY HLKPEEVDDF IRGQLVTNLP GVGHSMESKL
661 ASLGIKTCGD LQYMTMAKLQ KEFGPKTGQM LYRFCRGLDD RPVRTEKERK SVSAEINYGI
721 RFTQPKAEAE FLLSLSEELQ RRLEATGMKG KRLTLKIMVR KPGAPVETAK FGGHGICDNI
781 ARTVTLDQAT DNAKIIGKAM LNMFHTMKLN ISDMRGVGIH VNQLVPTNLN PSTCPSRPSV
841 QSSHFPSPGSY SVRDVFQVQK AKKSTEEHKK EVFRAAVDLE ISSASRTCTF LPPFPAHLPT
901 SPDTNKAESS GKWNGLHTPV SVQSRLNLSI EVSPSPQLDQ SVLEALPPDL REQVEQVCAV
961 QQAESHGDKK KEPVNGCNTG ILPQPVGTVL LQIPEPQESN SDAGINLIAL PAFSQVDPEV
1021 FAALPAELQR ELKAAVDQRR ROGENSTHQQ SASASVPKNP LLHLKAAVKE KKRNNKKKTI
1081 GSPKRIQSPL NNKLLNSPAK TLPGACGSPQ KLIDGFLKHE GPPAEKPLEE LSASTSGVPG
1141 LSSLQSDPAG CVRPPAPNLA GAVEFNDVKT LLREWITTIS DPMEEDILQV VKYCTDLIEE
1201 KDLEKLDLVI KYMKRLMQQS VESVWNMAFD FILDNVQVVL QQTYGSTLKV T
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Figure 9
Page 1 of 2

SEQ ID NO:17
Size: 2957
DNA APEI

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1 ctgcagatag cactgggaaa gacaccgcgg aactcccgcg agcgagaccc gccaaaggccc
61 ctccagggaac ctgtcttctt aacgtccagg gagcccagag caactcgcgc cttacattcg
121 tatccgtttt cctatctctt tcccgtggtc agcccagcct tctccactgt ttttttcttc
181 ttgcacagag ttagaatctt aagtcagtgt cacacaatgt gctgtgcac tggcacaacg
241 ataaacagcc gagggagggg tggggactaa gtgcctagag aattagagga gggaggcgag
301 gctaagcgtc cgtcacgtgg tgtcagacag accaatcacg cgcattcttc ggccacgaca
361 agcgcgcctc tgatcacgtg accagggtccg ctaccacagt ggggggtcag cgtgcaccct
421 tctttgtgct cgggttagga ggagctaggc tgccatcggg ccggtgcaga tacggggttg
481 ctcttttgct cataagaggg gcttcgctgg cagtctgaac ggcaagcttg agtcaggacc
541 cttaattaag atcctcaatt ggctggaggg cagatctcgc gagtagggtg caaggcacta
601 tgaatgatac tagtttcgtg ggtgaggggc tgaagggcct atgatgcacg gaggcgggga
661 aaggatttag agataacgtg gtttaaaggc gggacctggg gcggggagcg tccttggggg
721 gagtcttctc ccagccttag ctggtttcat gatttctttg cgtctgtagg caacgcggta
781 aaaatattgc ttcggtgggt gacgcggtag agctgcccac gggcggtcgt aacgggaatg
841 ccgaagcgta ggaaaaaagg agcgggtggc gaagacgggg atgagctcag gacaggtaag
901 ggaatgaaat cagcccttct tcttagaagc tgcggcgggg gtgtttgtca tcccttgat
961 gtacggtaag tacgggcca ctcatttttg cagggtttg tgaagaagtc gcaggaaccg
1021 taggctttcg ttgggtctat agttaacgcc ggatcgcagt tggaaaccac cagctttttg
1081 tcagtatata ttactcattt tatagagcca gaggccaaga agagtaagac ggccgcaaag
1141 aaaaatgaca aagaggcagc agggaggggc ccagccctgt atgaggaccc ccagatcag
1201 aaaacctcac ccagtggcaa acctgccaca ctcaagatct gctcttggaa tgtggatggg
1261 cttcgagcct ggattagaa gaaaggatta gatgtgagtg gaatttgagg gaaagagaca
1321 ttttttagta ttgaatggtc ttagggttta gtcacccctt ttctcgttt agccttcagg
1381 ctgttttatt tttctcctgc ccgtagttt ctgtggggct tcccagtc tggcagttgt
1441 atttctaaa tgtctgttcc ttcaactcca ttgccatttt cttttttagt gttctctctc
1501 cttcccagaa tgttgcaaaa acctcttcac tatacttctt ccattttatc ttctgcatt
1561 gcattccata tgaagcatgt cctccattcc attaacata gcttaaaatc ttagcttgcct
1621 atccactgcc tatagaaaaa acacatctcc ttggcatagc atgtaagact ttcttacctc
1681 tctatatttg ttttcattta tctagcttag aattgtttga atattgtgct gcttgactcg
1741 aactccttag gccaaagagc tgtttaacct gtgcgtatct atgacttagc atatagatta
1801 ttcaataaat gttctgctga attgataata cgttttccac ctttcttttc acttacagtg
1861 ggtaaggaa gaagcccag atatactgtg cttcaagag accaaatgtt cagagaacaa
1921 actaccagct gaacttcagg agctgcctgg actctctcat caatactggt cagctccttc
1981 ggacaaggaa gggtagagtg gcgtgggcct gctttccgc cagtgcacac tcaaagtttc
2041 ttacggcata ggtgagaccc tattgatgcc taatgcctga actcttcaaa accaattgct
2101 aattctctat ctctgcccc cctcttgatt gctttccctt ttcttatagt tttttatgct
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2221 ctgaatttga ctggtttgtg ctggtaacag catatgtacc taatgcaggc cgaggctcgg
2281 tacgactgga gtaccggcag cgtgggatg aagcctttcg caagtctctg aagggcctgg
2341 cttcccgaag gcccttgtg ctgtgtggag acctcaatgt ggcacatgaa gaaattgacc
2401 ttcgcaaccc caaggggaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct
2461 tcggggaatt actgcaggct gtgccactgg ctgacagctt taggcacctc taccccaaca
2521 caccctatgc ctacaccttt tggacttata tgatgaatgc tcgatccaag aatgttggtt
2581 ggcgccttga ttactttttg ttgtccact ctctgttacc tgcattgtgt gacagcaaga
2641 tccgttccaa ggccctcggc agtgatcact gtccatcac cctataccta gcaactgtgac
2701 accacccta aatcactttg agcctgggaa ataagcccc tcaactacca ttcttctttt
2761 aaacactctt cagagaaatc tgcattctat ttctcatgta taaaactagg aatcctccaa
2821 ccaggctcct gtgatagagt tcttttaagc ccaagatttt ttatttgagg gttttttgtt
2881 ttttaaaaaa aaattgaaca aagactacta atgactttgt ttgaattatc cacatgaaaa
2941 taaagagcca tagtttc
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Figure 9
Page 2 of 2

SEQ ID NO:18
Size: 318
PRT APE1

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1  MPKRGKKGAV AEDGDELRTE PEAKKSKTAA KKNDKEAAGE GPALYEDPPD QKTSPSGKPA
61  TLKICSWNVD GLRAWIKKKG LDWVKEEAPD ILCLQETKCS ENKLPAELQE LPGLSHQYWS
121 APSDKEGYSG VGLLSRQCPL KVSYGIGDEE HDQEGRVIVA EFDSFVLVTA YVPNAGRGLV
181 RLEYRQRWDE AFRKFLKGLA SRKPLVLCGD LNVAHEEIDL RNPKGNNKNA GFTPQEAQGF
241 GELLQAVPLA DSFRHLYPNT PYAYTFWTYM MNARSKNVGW RLDYFLLSHS LLPALCDSKI
301 RSKALGSDHC PITLYLAL
```


Figure 10

SEQ ID NO:19
Size: 1161
DNA CDK3

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1 ccacatggaa gctggaggag caaccgggag cgctgggctg gggtgcaaat tgcccagtgc
61 cttctgtttc ccaggcagct ctgtggccat ggatatgttc cagaaggtag agaagatcgg
121 agagggcacc tatggggtgg tgtacaaggc caagaacagg gagacagggc agctggtggc
181 cctgaagaag atcagactgg atttggagat ggaggggggtc ccaagcactg ccatcaggga
241 gatctcgctg ctcaaggaac tgaagcacc caacatcgtc cgactgctgg acgtggtgca
301 caacgagagg aagctctatc tgggtgttga gttcctcagc caggacctga agaagtacat
361 ggactccacc ccaggctcag agctccccct gcacctcatc aagagctacc tcttccagct
421 gctgcagggg gtgagtttct gccactcaca tcgggtcatc caccgagacc tgaagcccca
481 gaacctgctc atcaatgagt tgggtgccat caagctggct gacttcggcc tggctcgcgc
541 cttcgggggtg cccctgcgca cctacacca tgagggtggtg acactgtggt atcgcgcccc
601 cgagattctc ttgggcagca agttctatac cacagctgtg gatattctga gcattggttg
661 catcttttga gagatggtga ctcgaaaagc cctgtttcct ggtgactctg agattgacca
721 gctctttcgt atctttcgta tgctggggac acccagcgaa gacacatggc ccggggtcac
781 ccagctgcct gactataagg gcagcttccc taagtggacc aggaagggac tgaagagat
841 tgtgccaat ctggagccag agggcagggg cctgctcatg caactcctgc agtatgacct
901 cagccagcgg atcacagcca agactgcctt ggcccacccg ta~tttctcat cccctgagcc
961 ctccccagct gcccgccagt atgtgctgca gcgattccgc cattgagaat gtcaaggcca
1021 cactcagatc ctttctcgag cagcagctgc tgccccagct gcctcctacc cattgccaag
1081 agaggatgca tctggggaga gcaaagcact aaggaattca gcatcagcct gcagagggct
1141 gagtctgggt tagtcctgcc c

```

SEQ ID NO:20
Size: 305
PRT CDK3

```

1 MDMFQKVEKI GEGTYGVVYK AKNRETGQLV ALKKIRLDLE MEGVPSTAIR EISLLKELKH
61 PNIVRLLDVV HNERKLYLVF EFLSQDLKKY MDSTPGSELP LHLIKSYLFQ LLQGVSFCHS
121 HRVIHRDLKP QNLLINELGA IKLADFGLAR AFGVPLRITY HEVVTLWYRA PEILLGSKFY
181 TTAVDIWSIG CIFAEMVTRK ALFPGDSEID QLFRIFRMLG TPSEDTPWPGV TQLPDYKGSF
241 PKWTRKGLLE IVPNLEPEGR DLLMQLLQYD PSQRITAKTA LAHPYFSSPE PSPAARQYVL
301 QRFRH

```

Figure 11

SEQ ID NO:21

Size: 2297

DNA PIMI

```

1  gcgccgcac  ctggagggtt  ggatgctctt  gtccaaaatc  aactcgcttg  cccacctgcg
61  cgcgcgcgc  tgcaacgacc  tgcacgccac  caagctggcg  cggggcaagg  agaaggagcc
121 cctggagtcg  cagtaccagg  tggggccgct  actgggcagc  ggcggcttcg  gctcgggtct
181 ctcaggcatc  cgcgtctccg  acaacttgcc  ggtggccatc  aaacacgtgg  agaaggaccg
241 gatttccgac  tggggagagc  tgcctaattg  cactcgagtg  cccatggaag  tggctctgct
301 gaagaagggt  agctcgggtt  tctccggcgt  cattaggctc  ctggactggg  tcgagaggcc
361 cgacagtttc  gtctgatcc  tggagaggcc  cgagccgggt  caagatctct  tcgacttcat
421 cacggaaagg  ggagccctgc  aagaggagct  ggcccgcagc  ttcttctggc  aggtgctgga
481 ggccgtgcgg  cactgccaca  actgcggggt  gctccaccgc  gacatcaagg  acgaaaacat
541 ccttatcgac  ctcaatcgcg  gcgagctcaa  gctcatcgac  ttcgggtcgg  gggcgctgct
601 caaggacacc  gtctacacgg  acttcgatgg  gacccgagtg  tatagccctc  cagagtggat
661 ccgctaccat  cgctaccatg  gcaggtcggc  ggcagttctg  tccctgggga  tcctgctgta
721 tgatattggt  tgtggagata  ttcttttcga  gcatgacgaa  gagatcatca  gggggccagg
781 tttcttcagg  cagaggggtc  cttcagaatg  tcagcatctc  attagatggg  gcttggccct
841 gagaccatca  gataggccaa  ccttcgaaga  aatccagaac  catccatgga  tgcaagatgt
901 tctcctgccc  caggaaactg  ctgagatcca  cctccacagc  ctgtcgccgg  ggcccagcaa
961 atagcagcct  ttctggcagg  tctcccccct  tcttgtcaga  tgcccaggag  ggaagcttct
1021 gtctccagct  ttcccagata  ccagtgcac  gtctcgccaa  gcaggacagt  gcttgataca
1081 ggaacaacat  ttacaactca  ttccagatcc  caggcccctg  gaggctgcct  cccaacagtg
1141 ggggaagagt  actctccagg  ggtcctaggg  ctcaactcct  cccatagata  ctctcttctt
1201 ctcatagggt  tccagcattg  ctggactctg  aaatatcccg  ggggtggggg  gtgggggtgg
1261 gtcagaaccc  tgccatggaa  ctgtttcctt  catcatgagt  tctgctgaat  gccgcgatgg
1321 gtcaggtagg  ggggaaacag  gttgggatgg  gataggacta  gcaccatttt  aagtccctgt
1381 caccctctcc  gactctttct  gagtgccttc  tgtggggact  ccggctgtgc  tgggagaaat
1441 acttgaactt  gcctctttta  cctgctgctt  ctccaaaaat  ctgcctgggt  tttgttccct
1501 atttttctct  cctgtctctc  ctacccccct  ccttcatatg  aaaggtgcca  tggaagaggc
1561 tacagggcca  aacgctgagc  cactgcctct  tttttctcct  cctttagtaa  aactccgagt
1621 gaactgggtc  tccttttttg  tttttactta  actgtttcaa  agccaagacc  tcacacacac
1681 aaaaaatgca  caaacaatgc  aatcaacaga  aaagctgtaa  atgtgtgtac  agttggcatg
1741 gtagtatata  aaaagattgt  agtggatcta  atttttaaga  aattttgcct  ttaagttatt
1801 ttacctgttt  ttgtttcttg  ttttgaaaga  tgcgcattct  aacctggagg  tcaatgttat
1861 gtattttatt  atttatttat  ttggttccct  tctannnnnn  nnnnnngctg  ctgccttagt
1921 tttctttcct  cctttccctc  tctgacttgg  ggaccttttg  ggggagggtc  gcgacgcttg
1981 ctctgtttgt  ggggtgacgg  gactcaggcg  ggacagtgtc  gcagctccct  ggcttctgtg
2041 gggcccctca  cctacttacc  cagggtgggtc  ccggtctctg  ggggtgatgg  gaggggcatt
2101 gctgactgtg  tatataggat  aattatgaaa  agcagttctg  gatgggtgtg  cttccagatc
2161 ctctctgggg  ctgtgttttg  agcagcaggt  agcctgctgg  ttttatctga  gtgaaatact
2221 gtacagggga  ataaaagaga  tcttattttt  ttttttatac  ttggcgtttt  ttgaataaaa
2281 accttttgtc  ttaaaac

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SEQ ID NO:22

Size: 313

PRT PIMI

```

1  MLLSKINSLA  HLRARACNDL  HATKLAPGKE  KEPLESQYQV  GPLLGSGGFG  SVYSGIRVSD
61  NLPVAIKHVE  KDRISDWGEL  PNGTRVPM EV  VLLKKVSSGF  SGVIRLLDWF  ERPDSFVLIL
121 ERPEPVQDLF  DFITERGALQ  EELARSFFWQ  VLEAVRHCHN  CGVLHRDIKD  ENILIDLNRG
181 ELKLIDFGSG  ALLKDTVYTD  FDGTRVYSPP  EWIRYHRYHG  RSAAVWSLGI  LLYDMVCGDI
241 PFEHDEEII R  GQVFFRQRVS  SECQHLIRWC  LALRPSDRPT  FEEIQNHPPW  QDVLLPQETA
301 EIHLHLSLSPG  PSK

```

Figure 12
Page 1 of 2

SEQ ID NO:23
Size: 3178
DNA CDC7L1

```
1 gatctcttgg agacggcgac ccaggcatct ggggagccac agaagtcgta ctcccttaaa
61 ccctgctttg ctccccctgt ggatgtaacc ccttagctgg cattttgcat ctcaattggc
121 ttgtgatgga ggcgtctttg gggattcaga tggatgagcc aatggctttt tctccccagc
181 gtgaccggtt tcaggctgaa ggctctttta aaaaaaacga gcagaatttt aaacttgcag
241 gtgttaaaaa agatattgag aagctttatg aagctgtacc acagcttagt aatgtgttta
301 agattgagga caaaattgga gaaggcactt tcagctctgt ttatttggcc acagcacagt
361 tacaagtagg acctgaagag aaaattgctc taaaacactt gattccaaca agtcatccta
421 taagaattgc agctgaactt cagtgcctaa cagtggctgg ggggcaagat aatgtcatgg
481 gagttaaata ctgctttagg aagaatgac atgtagttat tgctatgcca taatctggagc
541 atgagtcggt tttggacatt ctgaattctc tttcctttca agaagtacgg gaatatatgc
601 ttaatctgtt caaagctttg aaacgcattc atcagtttgg tattgttcac cgtgatgtta
661 agcccagcaa ttttttatat aataggcgcc tgaaaaagta tgccttggtg gactttgggt
721 tggcccaagg aacctatgat acgaaaatag agcttcttaa atttgtccag tctgaagctc
781 agcaggaaag gtgttcacaa aacaaatccc acataatcac aggaacaag attccactga
841 gtggcccgat acctaaggag ctggatcagc agtccaccac aaaagcttct gttaaaagac
901 cctacacaaa tgcacaaatt cagattaaac aaggaaaaga cggaaaggag ggatctgtag
961 gcctttctgt ccagcgctct gtttttggag aaagaaattt caatatacac agtctcattt
1021 cacatgagag ccctgcagtg aaactcatga agcagtcaaa gactgtggat gtactgtcta
1081 gaaagtttagc aacaaaaaag aaggctatct ctacgaaagt tatgaatagt gctgtgatga
1141 ggaaaactgc cagttcttgc ccagctagcc tgacctgtga ctgctatgca acagataaag
1201 tttgtagtat ttgcctttca aggcgtcagc aggttgcccc tagggcaggt acaccaggat
1261 tcagagcacc agaggtcttg acaaagtgcc ccaatcaaac tacagcaatt gacatgtggg
1321 ctgcagggtg catatttctt tctttgctta gtggacgata tccattttat aaagcaagtg
1381 atgatttaac tgctttggcc caaattatga caattagggg atccagagaa actatccaag
1441 ctgctaaaac ttttgggaaa tcaatattat gtagcaaaga agttccagca caagacttga
1501 gaaaactctg tgagagactc aggggtatgg attctagcac tccaagtta acaagtgata
1561 tacaagggca tgcttctcat caaccagcta tttcagagaa gactgaccat aaagcttctt
1621 gcctcgttca aacacctcca ggacaatact cagggaaattc atttaaaaag ggggatagta
1681 atagctgtga gcattgtttt gatgagtata ataccaattt agaaggctgg aatgaggtag
1741 ctgatgaagc ttatgacctg cttgataaac ttctagatct aaatccagct tcaagaataa
1801 cagcagaaga agctttgttg catccatttt ttaaagatat gagcttgtga taatggatct
1861 tcatttaatg tttactgtta tgaggtagaa taaaaagaa tactttgtaa tagccacaag
1921 ttcttgttta gagaccagag caggattaat aatttatatt aacatttttag tgtttgggtg
1981 cactcttaa aatatagatt aagaatactt aaaatgcctg ggatagttct tgggactaac
2041 aacatgatct tctttgagtt aaacctacct aagtagattt taggtgggtt ccttatagg
2101 cagattttta gcttccttaa ttacctttca ctgacataca gaaaaaggag cagtttttagt
2161 ttttaattaat taaaattaac agatgtgatg aggattaaat gaatcaaaag acttaatttg
2221 tagattcttt tagagttatg agctaggtat agtttgggga aactcaacct ggtgctgggtg
2281 ctcttaacaa ttttgtaaat aaagaagata atttcctttt ctagaggtag atattaggcc
2341 ttttatgaac actaaaacaa tgaggaaatg ttggtcatgg ggcaaagtat cacttaaaat
2401 tgaattcatc cattttttaa aaacacttca tgaaagcatt ctggtgtgaa ttgccatttt
2461 tttcttactg gcttctcaat tttcttctt ctctgcccct acctaaaaca ttctctctcg
2521 aaattacatg gtgctgacca caaagtttct ggatgtttta ttaaatattg tacgtgttta
2581 cagttgggaa tttaaaataa tacatacact ggttgataaa gggaaagctgc aggaccaagg
2641 tgaagattga tagtccaaat gcttttcttt tttgagttgt atattttttc acaccatctt
2701 agatataatt aggtagctgc tgaaaggaaa agtgaataca gaattgacgg tattatttga
2761 gatttttctt ctgcgtagag ccatccagat ctctgtatcc tgttttgact aagtcttagg
2821 tgggttggga agacagataa tgaagtaggc aaagagaaaa ggaccaaga tagaggttta
2881 tattcagaaa tggatatata caatgacagc atatcaaact tcctatggga aaaagtctgg
2941 tgggtgggtc gctgacagat ttcccattta gtagtcatag aatacagaaa tagtttaggg
3001 acatgtattc attttgttat tttgagcatt gataggtcag tatatctacc taatctgttt
3061 ggtaagtata ggatatataa accattacca ttgatctgtc ttatgccata atcttaaaaa
3121 aaaattgaat gctcttgaat ttgtatatcc aataaagtta tccttttata aaaaaaaa
```

Figure 12
Page 2 of 2

SEQ ID NO:24
Size: 574
PRT CDC7L1

```
1 MEASLGIQMD EPMAFSPQRD RFQAEGLKK NEQNFKLAGV KKDIEKLYEA VPQLSNVFKI
61 EDKIGEGTFS SVYLATAQLQ VGPEEKIALK HLIPTSHPIR IAAELQCLTV AGGQDNVMGV
121 KYCFRKNNDHV VIAMPYLEHE SFLDILNSLS FQEVREYMLN LFKALKRIHQ FGIVHRDVKP
181 SNFLYNRRLLK KYALVDFGLA QGTHDTKIEL LKFVQSEAQQ ERCSQNKSHI ITGNKIPLSG
241 PVPKELDQQS TTKASVKRPY TNAQIQIKQG KDGKEGSVGL SVQRSVFGER NFNIHSSISH
301 ESPAVKLMKQ SKTVDVLSRK LATKKKAIST KVMNSAVMRK TASSCPASLT CDCYATDKVC
361 SICLSRRQQV APRAGTPGFR APEVLTKCPN QTTAIDMWSA GVIFLSLLSG RYPFYKASDD
421 LTALAQIMTI RGSRETIQAA KTFGKSILCS KEVPAQDLRK LCERLRGMDS STPKLTSDIQ
481 GHASHQPAIS EKTDHKASCL VQTPPGQYSG NSFKKGDSNS CEHCFDEYNT NLEGWNEVPD
541 EAYDLLDKLL DLNPASRITA EEALLHPFFK DMSL
```

Figure 13

SEQ ID NO:25
Size: 1427
DNA CDK7

```

1  tgggtgttgg aggcctttaag gtagctttaa attcgtgttg tcctgggagc tcgccctttt
61  cggctggagt cgggcctttac ggcgccggat ggctctggac gtgaagtctc gggcaaagcg
121 ttatgagaag ctggacttcc ttggggaggg acagtttgcc accgtttaca aggccagaga
181 taagaatacc aaccaaattg tcgccattaa gaaaatcaaa cttggacata gatcagaagc
241 taaagatggg ataaatagaa ccgccttaag agagataaaa ttattacagg agctaagtca
301 tccaaatata attggtctcc ttgatgcttt tggacataaa tctaattatta gccttgtctt
361 tgattttatg gaaactgata tagaggttat aataaaggat aatagtcttg tgctgacacc
421 atcacacatc aaagcctaca tgttgatgac tcttcaagga ttagaatatt tacatcaaca
481 ttggatccta catagggatc tgaaaccaa ccaactgttg ctagatgaaa atggagtctt
541 aaaactggca gattttggcc tggccaaatc ttttgggagc cccaatagag cttatacaca
601 tcaggttgta accagggtgg atcgggcccc cgagttacta tttggagcta ggatgtatgg
661 tgtagggtgt gacatgtggg ctggttgctg tatattagca gagttacttc taagggttcc
721 ttttttgcca ggagattcag accttgatca gctaacaaga atatttgaaa ctttgggcac
781 accaactgag gaacagtggc cggacatgtg tagtcttcca gattatgtga catttaagag
841 tttccctgga atacctttgc atcacatctt cagtgcagca ggagacgact tactagatct
901 catacaaggc ttattcttat ttaatccatg tgctcgaatt acgcccacac aggcactgaa
961 aatgaagtat ttcagtaatc ggccagggcc aacacctgga tgtcagctgc caagacaaaa
1021 ctgtccagtg gaaaccttaa aggagcaatc aaatccagct ttggcaataa aaaggaaaag
1081 aacagaggcc ttagaacaag gaggattgcc caagaaacta attttttaaa gagaacactg
1141 gacaacattt tactactgag ggaaatagcc aaaaaggcaa ataatggaaa aatagtaaac
1201 attaagtaaa tgctgtagaa gtgagtttgt aaatattcta cacatgtaaa atatgtaaaa
1261 ctatgggtta tttttattaa atgtatttta aaataaaaaa ttaattctgg tttttctgat
1321 tagagtccca aagtgagaaa agttcaatac tcttgaaatg tagaattgaa aatgcattag
1381 ggaaaactta ataaaaatta ttaccagtta tttggaaaaa aaaaaaa

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SEQ ID NO:26
Size: 346
PRT CDK7

```

1  MALDVKSRAK RYEKLDLFLGE GQFATVYKAR DKNTNQIVAI KKIKLHRSE AKDGINRTAL
61  REIKLLQELS HPNIIGLLDA FGHKSNISLV FDFMETDLEV IIKDNSLVLT PSHIKAYMLM
121 TLQGLEYLHQ HWILHRDLKP NNLLLDENG V LKLADFLAK SFGSPNRAYT HQVVTRWYRA
181 PELLFGARMY GVGVDMWAVG CILAEALLRV PFLPGDSDL QLTRIFETLG TPTEEQWPD
241 CSLPDYVTFK SFPGIPLHHI FSAAGDLDL LIQGLFLFNP CARITATQAL KMKYFSNRPG
301 PTPGCQLPRP NCPVETLKEQ SNPALAIKRK RTEALEQGGL PKKLIF

```

Figure 14

SEQ ID NO:27
Size: 2169
DNA CNK

```

1  ccgcctccga gtgccttgcg cggacctgag ctggagatgc tggccgggct accgacgtca
61  gaccccgggc gcctcatcac ggacccgcgc agcggccgca cctacctcaa aggccgcttg
121 ttgggcaagg ggggcttcgc ccgctgctac gaggccactg acacagagac tggcagcgcc
181 tacgctgtca aagtcatccc gcagagccgc gtcgccaagc cgcatacagc cgagaagatc
241 ctaaattgaga ttgagctgca ccgagacctg cagcaccgcc acatcgtgcg tttttcgcac
301 cacttttgagg acgctgacaa catctacatt ttcttgagac tctgcagccg aaagtccctg
361 gcccacatct ggaaggcccc gcacaccctg ttggagccag aagtgcgcta ctacctgcgg
421 cagatccttt ctggcctcaa gtacttgcac cagcgcggca tcttgaccg ggacctcaag
481 ttgggaaatt ttttcatcac tgagaacatg gaactgaagg tgggggattt tgggctggca
541 gcccggttgg agcctccgga gcagaggaag aagaccatct gtggcaccac caactatgtg
601 gctccagaag tgctgctgag acagggccac ggccctgaag cggatgtatg gtcactgggc
661 tgtgtcatgt acacgctgct ctgcgggagc cctccctttg agacggctga cctgaaggag
721 acgtaccgct gcatcaagca ggttccactac acgctgcctg ccagcctctc actgcctgcc
781 cggcagctcc tggccgccat ccttcggggc tcaccccgag accgcccctc tattgaccag
841 atcctgcgcc atgacttctt taccaagggc tacaccccg atcgactccc tatcagcagc
901 tgcgtgacag tcccagacct gacacccccc aaccagcta ggagtctgtt tgccaaagtt
961 accaagagcc tctttggcag aaagaagaag agtaagaatc atgccagga gagggatgag
1021 gtctccggtt tgggtgagcg cctcatgcgc acatocgttg gccatcagga tgccaggcca
1081 gaggctccag cagcttcttg cccagccctt gtcagcctgg tagagacagc acctgaagac
1141 agctcaccac gtgggacact ggcaagcagt ggagatggat ttgaagaagg tctgactgtg
1201 gccacagtag tggagtgcgc cctttgtgct ctgagaaatt gtatagcttt catgccccca
1261 gcggaacaga acccgcccc cctggccag ccagagcctc tgggtggtgg cagcaagtgg
1321 gttgactact ccaataagtt cggttttggg tatcaactgt ccagccgccc tgtggtgtg
1381 ctcttcaacg atggcacaca tatggccctg tcggccaaca gaaagactgt gactacaat
1441 cccaccagca caaagcactt ctcttctctc gtgggtgctg tgccccgggc cctgcagcct
1501 cagctgggta tctgcggtg cttgcctctc tacatggagc agcactcat gaaggggtgga
1561 gatctgcca gtgtggaaga ggtagaggta cctgctccgc ccttgtgctg gcagtgggtc
1621 aagacggatc aggtctctct catgtgtgtt agtgatggca ctgtccaggt gaacttctac
1681 ggggaccaca ccaagctgat tctcagtggc tgggagcccc tcttgtgac ttttgtggcc
1741 cgaaatcgta gtgcttgtag ttacctcgct tcccacctc ggcagctggg ctgctctcca
1801 gacctgcggc agcgactccg ctatgctctg cgctgctcc tctggccctt gcctttgtgg
1861 gaccaagcc ctgaaggcct gaggcctgtg cctgtcaggc tctggccctt gcctttgtgg
1921 ccttccccct tcctttggtg cctcactggg ggctttgggc cgaatcccc aggggaatcag
1981 ggaccagctt tactggagtt gggggcggct tgtcttcgct ggctctacc ccatctccaa
2041 gataagcctg agccttagct cccagctagg gggcggtatt tatggaccac ttttatttat
2101 tgtcagacac ttattttatt ggatgtgagc cccagggggc ctctctctag gataataaac
2161 aattttgca

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SEQ ID NO:28
Size: 607
PRT CNK

```

1  MLAGLPTSDP GRLITDPRSG RTYLKGRLLG KGGFARCYEA TDTETGSAYA VKVIPQSRVA
61  KPHQREKILN EIELHRDLQH RHIVRFSHHF EDADNIYIFL ELCSRKSLAH IWKARHTLLE
121 PEVRYYLROI LSGLKYLHQR GILHRDLKLG NFFITENMEL KVGDFGLAAR LEPPEQRKKT
181 ICGTPNYVAP EVLLRQGHGP EADVWSLGCV MYTLLCGSPP FETADLKETY RCIKQVHYTL
241 PASLSLPAEQ LLAAILRASR RDRPSIDQIL RHDFFTKGYT PDRLPISSCV TVPDLTPPNP
301 ARSLFAKVTK SLFGRKKKSK NHAQERDEVS GLVSGLMRTS VGHQDARPEA PAASGPAPVS
361 LVETAPEDSS PRGTLASSGD GFEEGLTVAT VVESALCALR NCIAFMPPAE QNPAPLAQPE
421 PLVWVSKWVD YSNKFGFGYQ LSSRRVAVLF NDGTHMALSA NRKTVHYNPT STKHFSFSVG
481 AVPRALQPQL GILRYFASYM EQHLMKGGDL PSVEEVEVPA PPLLLQWVKT DQALLMLFSD
541 GTVQVNFYGD HTKLILSGWE PLLVTFVARN RSACTYLASH LRQLGCSPDL RQRLRYALRL
601 LRDRSPA

```

Figure 15

SEQ ID NO:29
Size: 1321
DNA PRL-3

```

1  tgactatcca gctctgagag acgggagttt ggagttgccc gctttacttt ggttgggttg
61  gggggggcgg cgggctgttt tgttcctttt cttttttaag agttgggttt tcttttttaa
121 ttatccaaac agtgggcagc ttctccccc acaccaagt atttcacaa tatttgtagc
181 gggatatggg gtgggttttt aaatctcggt tctcttgga aagcacagg atctcggtct
241 cctcattttt tgggggtgtg tggggacttc tcaggtcgtg tcccagcct tctctgcagt
301 cccttctgcc ctgccgggcc cgtcgggagg cgccatggct cggatgaacc gcccggcccc
361 ggtggagggt agctacaaac acatgcgctt cctcatcacc cacaaccca ccaacgccac
421 gctcagcacc ttcattgagg acctgaagaa gtacggggct accactgtgg tgcgtgtgtg
481 tgaagtgacc tatgacaaaa cgccgctgga gaaggatggc atcaccttg tggactggcc
541 gtttgacgat ggggcgcccc cgcccggcaa ggtagtggaa gactggctga gcctggtgaa
601 ggccaagttc tgtgaggccc ccggcagctg cgtggctgtg cactgcgtgg cgggcctggg
661 ccggaagcgc cgcggagcca tcaacagcaa gcagctcacc tacctggaga aataccggcc
721 caaacagagg ctgcggttca aagaccaca cacgcacaag acccggtgct gcgttatgta
781 gctcaggacc ttggtgggct ctggtcgtca tgtaggtcag gacctggct ggacctggag
841 gccctgcccc gccctgctct gccagccca gcaggggctc caggccttg ctggccccac
901 atcgctttt cctccccgac acctccgtgc acttgtgtcc gaaggagcag gagccctctg
961 ggccctgggt ggccctctgg ccctttctcc tgtctccgc actccctctg gcggcgctgg
1021 ccgtggctct gtctctctga ggtgggtcgg gcgccctctg ccgccccct cccacaccag
1081 ccaggctggt ctctcttagc ctgtttgttg tggggtgggg gtatatattg taaccactgg
1141 gccccagcc cctcttttgc gacccttgt cctgacctgt tctcggcacc ttaaattatt
1201 agaccccggt gcagtcaggt gctccggaca ccgaaggca ataaaacagg agccgtgaaa
1261 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1321 a

```

SEQ ID NO:30
Size: 148
PRT PRL-3

```

1  MARMNRPAPV EVSYKHMRF ITHNPTNATL STFIEDLK KY GATTVVRVCE VTYDKTPLEK
61  DGITVVDWPF DDGAPPPGKV VEDWLSLVKA KFCEAPGSCV AVHCVAGLGR KRRGAINSKQ
121 LTYLEKYRPK QLRFKDPHT HKTRCCVM

```

Figure 16
Page 1 of 2

SEQ ID NO:31
Size: 3696
DNA STK2 (NEK4)

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1  ggatcgctat  ggcagcggcg  tcgtcgcggg  ccgggcccga  gcaatcccgc  ccggggcccg
61  ctgcctcaac  agccgcccc  actgccccct  ctcgggcatg  aaccgagctt  cttggtgocg
121  cccgctgccc  taccgcccgc  tgccgcccga  tcccgaactc  gggccagcgc  tgggaacatg
181  cccctggccg  cctactgcta  cctgcgggtc  gtgggcaagg  ggagctatgg  agaggtgacg
241  cttgtgaagc  accggcggga  cggcaagcag  tatgtcatca  aaaaactgaa  cctccgaaat
301  gcctctagcc  gagagcggcg  agctgctgaa  caggaagccc  agctcttgct  tcagttgaag
361  catcccaaca  ttgtcaccta  caaggagtca  tgggaaggag  gagatgggtc  gctctacatt
421  gtcatgggct  tctgtgaagg  aggtgatttg  taccgaaagc  tcaaggagca  gaaagggcag
481  cttctgcctg  agaatcaggt  ggtagagtgg  tttgtacaga  tcgcatggc  tttgcagtat
541  ttacatgaaa  aacacatcct  tcatcgagat  ctgaaaactc  aaaaatgtct  cctaacaaga
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661  atggctagca  ccctcattgg  cacaccctac  tacatgagcc  ctgaattgtt  ctcaaacaaa
721  ccctacaact  ataagtctga  tgtttgggct  ctaggatgct  gtgtctatga  aatggccacc
781  ttgaagcatg  ctttcaatgc  aaaagatatg  aattctttag  tttatcggat  tattgaagga
841  aagctgccac  caatgccaa  agattacagc  ccagagctgg  cagaactgat  aagaacaatg
901  ctgagcaaaa  ggctgaaga  aaggccgtct  gtgaggagca  tcctgaggca  gccttatata
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1021  aaaaatgggtg  actctcaatc  caagcctttt  gctacagtgg  tttctggaga  ggcagatatc
1081  aatcatgaag  taatccaccc  ccaaccactc  tcttctgagg  gctcccagac  atatataatg
1141  ggtgaaggca  aatgtttgtc  ccaggagaaa  cccagggcct  ctggtctctt  gaagtcacct
1201  gccagtctga  aagcccatac  ctgcaaacag  gacttgagca  ataccacaga  actagccaca
1261  atcagtagcg  taaatatgta  catcttacct  gcaaaaggga  gggattcagt  gagtgatggc
1321  tttgttcagg  agaatcagcc  aagatatttg  gatgcctcta  atgagttagg  aggtatatgc
1381  agtatttctc  aagtgggaag  ggagatgctg  caggacaaca  ctaaatccag  tgcccagcct
1441  gaaaacctga  ttcccatgtg  gtccctctgac  attgtcactg  gggaaaagaa  tgaaccagtg
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1621  agtgattctc  cagcctcagc  ctcccagagta  gctgggatta  caggcgtgtg  ccaccagccc
1681  caggatcaag  ttgctgggtg  atgtattata  gaaaaacagg  gcagaatcca  cccagattta
1741  cagccacaca  actctgggtc  tgaaccttcc  ctgtctcgac  agcgacggca  aaagaggaga
1801  gaacagactg  agcacagagg  ggaaaagaga  caggctccgca  gagatctctt  tgctttccaa
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1981  agcagtga  tgtcatcatc  aaaggatcga  ccattatcag  ccagagagag  gaggcgacta
2041  aagcagtcac  aggaagaaat  gtctcttcca  ggccttcag  tgaggaaagc  gtctctgagt
2101  gtagcagggc  caggaaaacc  ccaggaagaa  gaccagccct  tgctgcccgc  acggctctcc
2161  tctgactgca  gcgtcactca  ggaaaggaaa  cagattcatt  gtctgtctga  ggatgagtta
2221  agttcttcta  caagttcaac  tgataagtca  gatggggatt  acggggaagg  gaaaggtcag
2281  acaaatgaaa  ttaatgcctt  ggtacaattg  atgactcaga  cctgaaact  ggattctaaa
2341  gagagctgtg  aagatgtccc  ggtagcaaac  ccagtgtcag  aattcaaaact  tcatcggaag
2401  tatcgggaca  cactgatact  tcatgggaag  gttgcagaag  aggcagagga  aatccatttt
2461  aaagagctac  cttcagctat  tatgccaggt  tctgaaaaga  tcaggagact  agttgaagtc
2521  ttgagaactg  atgtaattcg  tggcctggga  gttcagcttt  tagagcaggt  gtatgatctt
2581  ttggaggagg  aggatgaatt  tgatagagag  gtacgtttgc  gggagcacat  gggtgaaaag
2641  tatacaactt  acagtgtgaa  agctcgccag  ttgaaatttt  ttgaagaaaa  catgaatttt
2701  tgagcatttg  tcctaactcg  ctgccagaat  taaagacct  tttttagagg  attttggtct
2761  aaaaagcaag  ggcaaacagt  catttggaag  ccactcacca  ctgttttata  tctctttttt
2821  atatctcttt  ggcgtttccc  tacagaaaag  aaattggaca  gaacagaata  atatgaagca
2881  ggatcacaaa  agaaaaaaa  ctttggtctt  catattctct  ttgtgaggag  aaatctgttg
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3001  ttttaaggta  ctaattaaact  taaacacaga  gctataaaat  gctggattga  aaattttata
3061  ttgtaatgta  gagataaaag  cagtaggaga  aacaaatgac  ataatatgtc  gtcataattc
3121  ctgctattgt  taataacctt  aaggagtagt  tgataaatta  taaaatttta  aaaagtcaat
3181  tcagttctag  aaatagattt  aaagaatatg  aagttctatc  tagtacttga  gcagctgtat
```


Figure 16
Page 2 of 2

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3241 ttcttttcta cacattgatg gacttttaaat attttatttct catttaatat aaacctcatc
3301 tagggatatat acaaattaaa actgagacac attggctttg taaatcagta tgtttttaca
3361 taatgggtttt gttagatttta tttttccatc agtgaaaaca tttcttaagc acaaatttca
3421 ttcccattta agcaatttgt aagcaaagtc cagggtccatt tagtttttgg atatatttaa
3481 tgtttgctct ctgaagtttg tcttcagtga ctgtaagata ttagttgtct ttccatgttt
3541 taaatgtatg attatatagc acatatttta ttagttgttt aataagaggt aataccatc
3601 taggaaagaa attttatgaa gttaaataca agtcttgaat agtacatttt cacttctgta
3661 ttcgagggac tctaaaaata aatattgtct cagaaa
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SEQ ID NO:32
Size: 841
PRT STK2 (NEK4)

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1 MPLAAYCYLR VVGKGSYGEV TLVKHRRDGK QYVIKKLNLN NASSRERRAA EQEAQLLSQL
61 KHPNIVTYKE SWEGGDGLLY IVMGFCEGGD LYRKLKEQKG QLLPENQVVE WfvQIAMALQ
121 YLHEKHILHR DLKTQNVFLT RTNIIKVGDL GIARVLENHC DMASTLIGTP YYMSPELFSN
181 KPYNYKSDVW ALGCCVYEMA TLKHAFNAKD MNSLVYRIIE GKLPMPRPDY SPELAELIRT
241 MLSKRPEERP SVRSILRQPY IKRQISFFLE ATKIKTSKNN IKNGDSQSKP FATVVSGEAE
301 SNHEVIHPQP LSSEGSQTYI MGEKGCLSQE KPRASGLLKS PASLKAHTCK QDLSNTTELA
361 TISSVNIDIL PAKGRDSVSD GFVQENQPRY LDASNELGGI CSISQVEEEM LQDNTKSSAQ
421 PENLIPMWSS DIVTGEKNEP VKPLQPLIKE QKPKDQSLAL SPKLECSGTI LAHSNLRLLG
481 SSDSPASASR VAGITGVCHH AQDQVAGECI IEKQGRIHPD LQPHNSGSEP SLSRQRRQKR
541 REQTEHRGEK RQVRRDLFAF QESPPRFLPS HPIVGKVDVT STQKEAENQR RVVTGSVSSS
601 RSSEMSSSKD RPLSARERRR LKQSQEEMSS SGPSVRKASL SVAGPGKPQE EDQPLPARRL
661 SSDCSVTQER KOIHCLSEDE LSSSTSSTDK SDGDYGEKGQ QTNEINALVQ LMTQTLKLDS
721 KESCEDVPVA NPVSEFKLHR KYRDTLILHG KVAEEAEEIH FKELPSAIMP GSEKIRRLVE
781 VLRTDVIRGL GVQLLEQVYD LLEEDEFDR EVRLREHMGE KYTTYSVKAR QLKFFEENMN
841 F
```

Figure 17

SEQ ID NO:33
Size: 1513
DNA NKIAMRE

```

1 atggagatgt atgaaaccct tggaaaagtg ggagaggggaa gttacggaac agtcatgaaa
61 tgtaaacata agaatactgg gcagatagtg gccattaaga tattttatga gagaccagaa
121 caatctgtca acaaaattgc gatgagagaa ataaagtttc taaagcaatt tcatcacgaa
181 aacctgggtca atctgattga agtttttaga cagaaaaaga aaattcattt ggtatttgaa
241 tttattgacc acacagtatt agatgagtta caacattatt gtcatggact agagagtaag
301 cgacttagaa aatacctctt ccagatcctt cgagcaattg actatcttca cagtaataat
361 atcattcatc gagatataaa acctgagaat attttagtat ccagtcagg aattactaag
421 ctctgtgatt ttggttttgc acgaacacta gcagctcctg gggacattta tacggactat
481 gtggccacac gctggtatag agctcccgaa ttagtattaa aagatacttc ttatggaaaa
541 cctgtggata tctgggcttt gggctgtatg atcattgaga tggccactgg aaatccctat
601 cttcctagta gttctgattt ggatttactc cataaaattg ttttgaaagt gggcaatttg
661 tcacctcact tgcagaatat cttttccaag agccccattt ttgctggggg agttcttctt
721 caagttcaac accccaaaaa tgcaagaaaa aaatatccaa agcttaatgg attgttggca
781 gatatagttc atgcttgttt acaaattgat cctgctgaca ggatatcatc tagtgcctt
841 ttgcatcatg agtattttac tagagatgga tttattgaaa aattcatgcc agaactgaaa
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1141 ggacttggtc aacaggatgc aaatgaaaat gttcatccta tgtctccaga tacaaaactt
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SEQ ID NO:34
Size: 455
PRT NKIAMRE

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1 MEMYETLGKV GEGSYGTVMK CKHKNTGQIV AIKIFYERPE QSVNKIAMRE IKFLKQFHHE
61 NLVNLIEVFR QKKKIHLVFE FIDHTVLDEL QHYCHGLESK RLRKYLQIL RAIDYLSNN
121 IHRDIKPEN ILVSQSGITK LCDFGFARTL AAPGDIYTDY VATRWYRAPE LVLKDTSYGK
181 PVDI WALGCM I IEMATGNPY LPSSSDL DLL HKIVLKVGNL SPHLQNI FSK SPIFAGV VLP
241 QVQHPKNARK KYPKLNGLLA DIVHACLQID PADRISSSDL LHHEYFTRDG FIEKFMP ELK
301 AKLLQEAKVN SLIKPKESSK ENELRKDERK TVYTNLLSS SVLGEEIEKE KKPKEIKVRV
361 IKVKGGRGDI SEPKKKEYEG GLGQQDANEN VHPMSPDTKL VTIEPPNPIN PSTNCNGLKE
421 NPHCGGSVTM PPINLTNSNL MAANLSSNLF HPSVR

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Figure 18
Page 1 of 2

SEQ ID NO:35
Size: 3504
DNA HBO1

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1 gccgctgccc gaatcggaa cgtcggggccg cagccgcccg caatgccgcg aaggaagagg
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121 acagacagtt cagaaagtga tggcacatcc cgacgatctg ctcgagtcac ccgctcctca
181 gccaggctaa gccagagttc tcaagattcc agtcctgttc gaaatctgca gtcttttggc
241 actgaggagc ctgcttactc taccagaaga gtgaccgcta gtcagcagca gcctacccca
301 gtgacaccga aaaaatacc ctttcggcag actcgttcat ctggttcaga aactgagcaa
361 gtggttgatt tttcagatag agaaactaaa aatacagctg atcatgatga gtcaccgcct
421 cgaactccaa ctggaaatgc gccttcttct gagtctgaca tagatatctc cagccccaat
481 gtatctcacg atgagagcat tgccaaggac atgtccctga aggactcagg cagtgatctc
541 tctcatcgcc ccaagcgccg tcgcttccat gaaagctaca acttcaatat gaagtgtcct
601 acaccaggct gtaactctct aggacacctt acaggaaaac atgagagaca tttctccatc
661 tcaggatgcc cactgtatca taacctctca gctgacgaat gcaaggtgag agcacagagc
721 cgggataagc agatagaaga aaggatgctg tctcacaggc aagatgacaa caacaggcat
781 gcaaccaggc accaggcacc aacggagagg cagcttcgat ataaggaaaa agtggctgaa
841 ctcaggaaga aaagaaattc tggactgagc aaagaacaga aagagaaata tatggaacac
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961 ttggatcttt tccgaagagc acaagcccgg gcttcagagg atttgagaaa gtttaaggctg
1021 caaggccaaa tcacagaggg aagcaacatg attaaaaaa ttgcttttgg ccgctatgag
1081 cttgatacct ggtatcattc tccatatect gaagaatatg cacggctggg acgtctctat
1141 atgtgtgaat tctgtttaaa atatatgaag agccaaacga tactccgccc gcacatggcc
1201 aaatgtgtgt ggaaacaccc acctggtgat gagatatatc gcaaagggtc aatctctgtg
1261 tttgaagtgg atggcaagaa aaacaagatc tactgccaaa acctgtgcct gttggccaaa
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2461 aaatactttt gaagagtttc ccagggacta gtcattggtaa tagcatataa ttgatctgaa
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Figure 18
Page 2 of 2

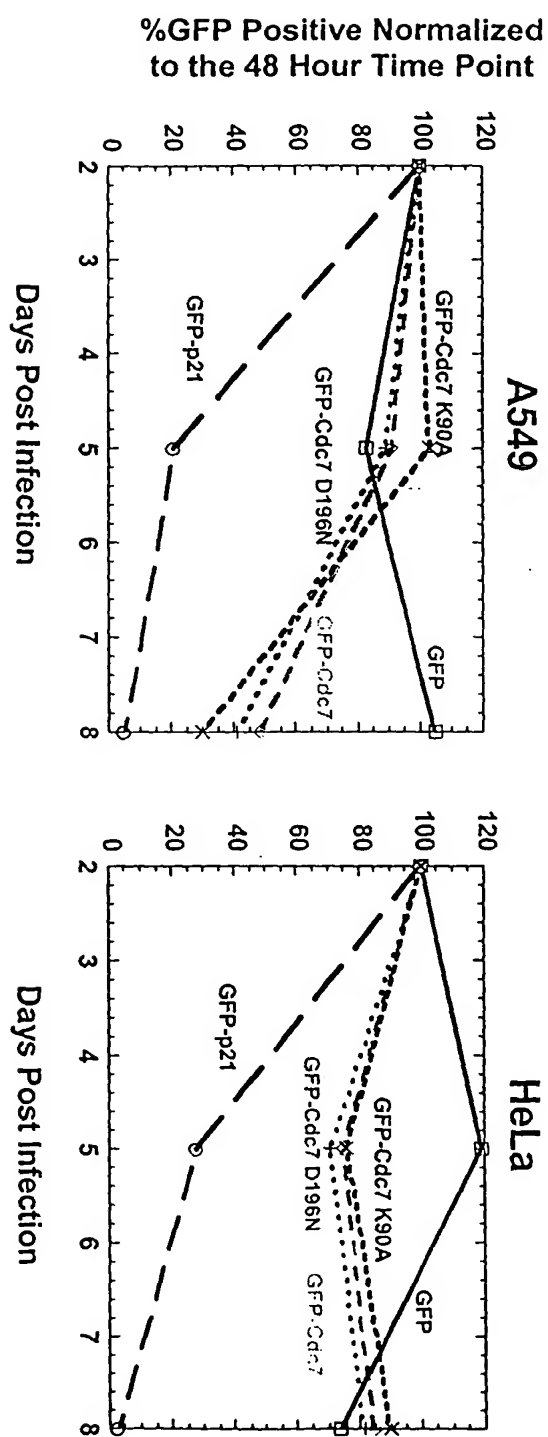
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SEQ ID NO:36
Size: 611
PRT HBO1

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1  MPRRKRNAGS SSDGTEDSDF STDLEHTDSS ESDGTSRRSA RVTRSSARLS QSSQDSSPVR
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121 HDESPRPTPT GNAPSSSEDI DISSPNVSHD ESIKDMSLK DSGSDLSHRP KRRRFHESYN
181 FNMKCPTPGC NSLGHLTGKH ERHFSISGCP LYHNLSADEC KVRAQSRDKQ IEERMLSHRQ
241 DDNNRHATRH QAPTERQLRY KEKVAELRKK RNSGLSKEQK EKYPMEHRQTY GNTREPLEN
301 LTSEYDLDLF RRAQARASED LEKLRLQGQI TEGSNMIKTI AFGRYELDTW YHSPYPEEYA
361 RLGRLYMCEF CLKYMKSQTI LRRHMAKCVW KHPPGDEIYR KGSISVFEVD GKKNKIYCQN
421 LCLLAKLFLD HKTLYYDVEP FLFYVMTEAD NTGCHLIGYF SKEKNSFLNY NVSCILTMPQ
481 YMRQGYGKML IDFSYLLSKV EEKVGSPERP LSDLGLISYR SYWKEVLLRY LHNFGQKEIS
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601 SCLKWTPPKG T
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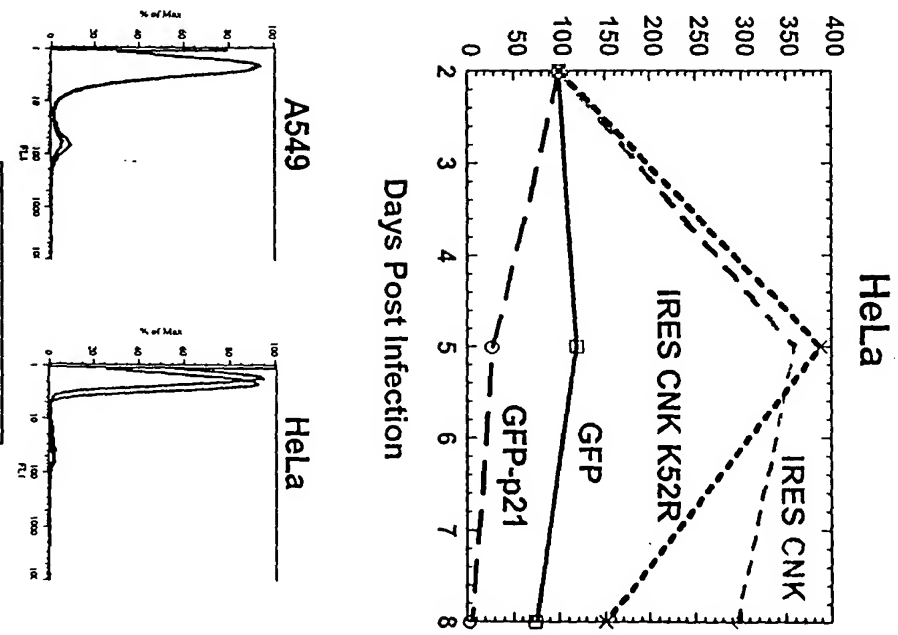
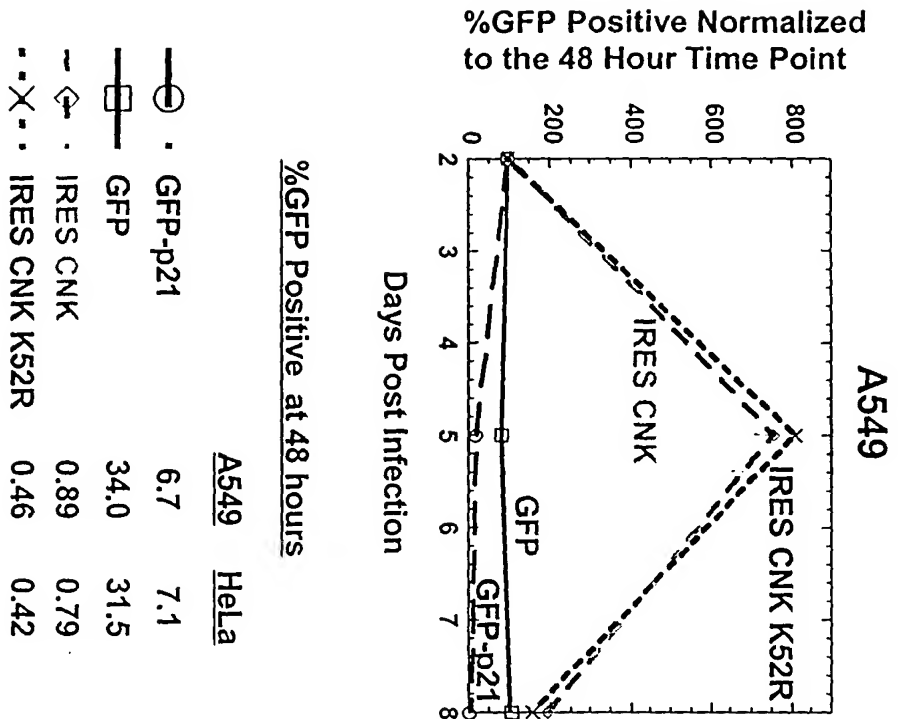
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PLC-beta 1	NM_01519/NP_056007	RbAp48 ip	Phospholipase
PTK2(FAK)	L05186/AAA35819	14-3-3 YTH	Y kinase
PTK2b(FAK2)	L49207/Q14289	XIAP YTH	Y kinase
CK2	NM_001895/NP_001886	DNAPK YTH	S/T kinase
cMET	J02958/AAA59591	RbAp48 ip	Y kinase
FEN1	NM_004111/NP_004102	PCNA YTH	Endonuclease
REV1	AF206019/AAF18986	Myt1 YTH	dCMP transferase
APE1:	X66133/S34422	p16 YTH	Endonuclease
CDK3:	NM_001258/NP_001249	CKS2, HSPC YTH	S/T kinase
PIM1	M16750/AAA60089	p21 ip	S/T kinase
CDC7L1	NM_003503/NP_003494	Apoptin, GADD34 YTH + bioinf	S/T kinase
CDK7	NM_001799/NP_001790	CIP1 YTH+bioinf	S/T kinase
CNK	NM_004073/NP_004064	DNAPKF7 YTH	S/T kinase
PRL-3	NM_007079/NP_009010	Myt1 YTH	Y phosphatase
STK2	XM_003216/XP_003216	p73 YTH	S/T kinase
NKIAMRE	AF130372/AAF36509	RbAp48 ip	S/T kinase.
HBO1	NM_007067/NP_008998	p66H YTH	Histon acetylase

FIGURE 19



%GFP Positive at 48 Hours	
A549	HeLa
● GFP-p21	7.1
□ GFP	31.5
◇ GFP-Cdc7	1.27
× GFP-Cdc7 K90A	0.82
+ GFP-Cdc7 D196N	1.12

FIGURE 20



%GFP Positive at 48 hours

	A549	HeLa
○ — GFP-p21	6.7	7.1
□ — GFP	34.0	31.5
◇ — IRES CNK	0.89	0.79
× — IRES CNK K52R	0.46	0.42

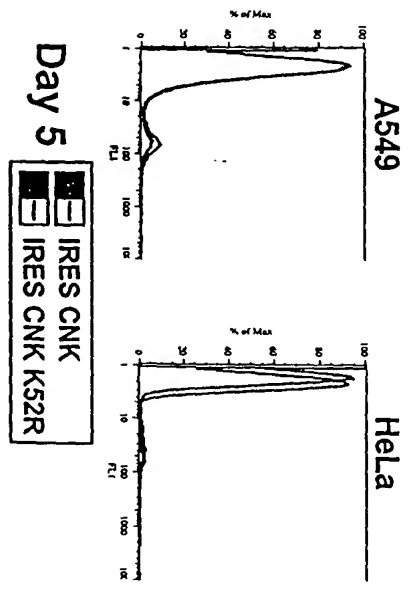
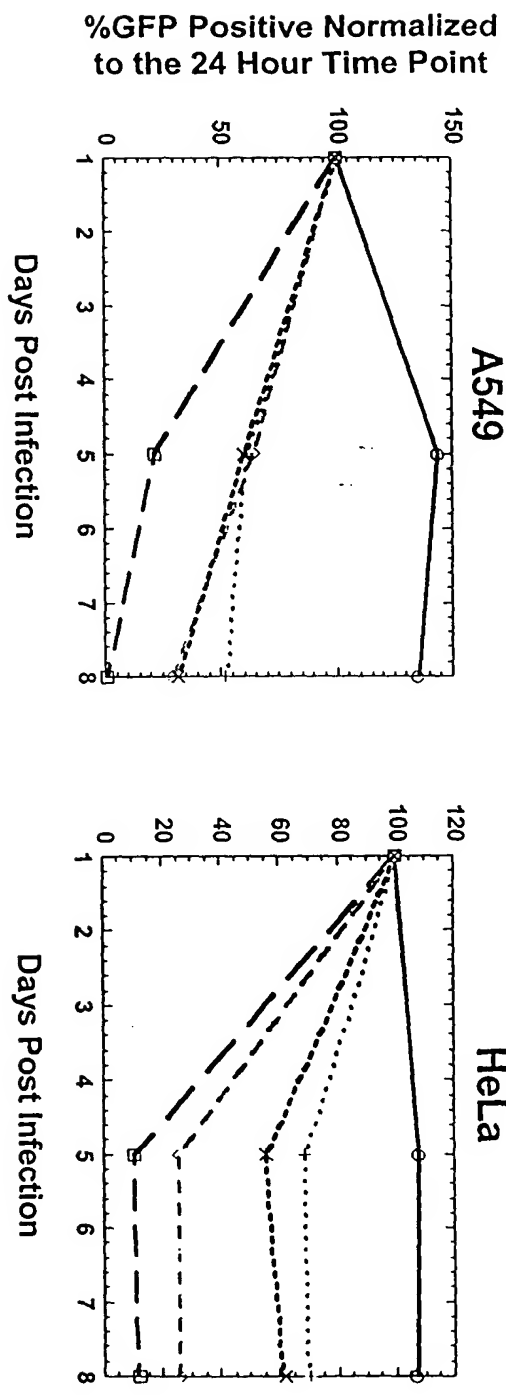


FIGURE 21



%GFP Positive at 24 Hours

	<u>A549</u>	<u>HeLa</u>
—■— GFP	52.8	59.0
—●— GFP-p21	11.0	23.1
—◇— GFP-STK2S	9.99	9.65
—×— GFP-STK2S K35A	9.23	7.88
···+··· GFP-STK2S D149A	7.35	6.56

FIGURE 22

Point mutant : K90A, D196N - K90A corresponds to a mutation in the catalytic residue in the kinase domain
D196N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

CDC7L1	MEASLGIMDEPMASFSPQRDRFQAEGLKKNQNFKLAGVKKDIEKL YEAVPOLSNVFKI
CDC7Sc	-----MTSKTKNIDDIPEIKEEMIQLYHDLPGIENEYKL
	: * : : * : : * : * : *
CDC7L1	EDKIGEGTFSSVYLAT-----AQLQVPEEKALKHLIPTSHPIRIAAEQCLT
CDC7Sc	IDKIGEGTFSSVYKAKDITGKITKKFASHFWNYSNVYALKKIYVTSPPQRIYNELNLLY
	***** * : : : * : * : *
CDC7L1	VAGGQDNVMGVKCYCFRKNQDVVIAMPYLEHESFLDILNSLSQAEVREYMLNLFKALKRIH
CDC7Sc	IMTGSSRVAPLCDAKRVRDQVIAVLPYPHEEFRTFYRDLPPIGIIKKYIWELLRALKFVH
	: * : : * : : * : * : *
CDC7L1	QFGIVHRDVKPSNFLYNRRLKKYALVDFGLAAGTHDTKIELLKVFQSEAAQDERCSQNKSH
CDC7Sc	SKGIIHRDIKPTNLFNLELGRGVLVDFGLAEAQMDYKSMISSQND-----
	***** * : : * : *
CDC7L1	IITGNKIPLSGVPVKELDQAQSTTKASVKRPYTNAQIAIKQKGDKEGSGVGLSVQRSVFGE
CDC7Sc	-----YDN-----YANTNHDGGYSMRNHEQFCPC
	: : : * : : *
CDC7L1	RNFNIHSSISHESPAVKLMKQSKTVDVLSRKLATKKKAISTKYMNSAVMRKTASSCPASL
CDC7Sc	IMRNQYSPNSHNQTPMVTIQNGKVHLN-----
	* : * : * : *
CDC7L1	TCDCYATDKVCSICLSRQQAVAPRAGTGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLS
CDC7Sc	NVNGVDLTKGYPKNETRIKIRANRAGTRGFRAPVLMKCGAAGSTKIDIWSVGVILLSLG
	* : * : * : * : * : *

FIGURE 23

Point mutant : K52R and D146A - the catalytic residue in the kinase domain.
(J. Biol. Chem., Vol. 276, Issue 46, 43305-43312, November 16, 2001. PMID: 11551930)

kinase: domain 1 of 1, from 23 to 275: score 309.5, E = 2.5e-90

```

*->yelleklGegsfGkVykakhkdktgkiVAVkIlkkekesikek...r
Y +++ lG+G+f+++y+++ +tg +AvK+++ + + k+++++
query 23 YLKGRLGKGGFARCYEATDT-ETGSAYAVKVIP-QSRVAKPHGREK 67

flreiqlkrlshpNivrligvfedtdhlylvmEymegdlfdylrrng
+l+Ei++++ L+H +Ivr+ + fe + d+++y+ +E++ +L+++++++
query 68 ILINEIELHRDLQHRHIVRFSHHFE-DADNITYIFLELCSRKSLAHIWKARH 116

gplsekeakkialQilrgleyLHsngivHRDLKpenILldendgtvkiad
+ l e+++ + +Qil+Gl+YLH +gi+HRDLK N++++en + +K++D
query 117 TLL-EPEVRYYLRLQILSGELKYLHQRGILHRDLKGNFFITEN-MELKVGD 164

FGLARlle.ssskltttfvGTPwYmmAPEvilegrgysskvdvWSlGvily
FGLA+ le++ ++++t++GTP+Y+ APEv l+++g+++++DvWSlG+++Y
query 165 FGLARLEPPEQRKKTICGTPNVV-APEV-LLRQHGPEADVWSlGCVMY 212

ElitgspIfpgadlpafTgdevdqliifvklpfsdelpktidpleel
ll+g +Pf+ + l+e
query 213 TLLCG-----SPPFE-----TADLKET 229

friikrpglrIplpsncSeelkdlkkclnkdPskRpGsatakeilnhpwf
+r ik+ ++ lp ++S ++++Ll +L+ P +Rp ++ +il h +f
query 230 YRCIKQ--VHYTLPASLSLPARQLLAAILRASPRDRP---SIDQILRHDF 275

```

FIGURE 24

Point mutants : K35A and D149A - the catalytic residue in the kinase domain.

kinase: domain 1 of 1, from 6 to 261: score 288.9, E = 4.2e-84
 *->yel1ek1GegsfGkykakhkdtgkiVAvkilkkikesiek...r
 Y 1+++G+Gs+G+V ++kh+ +gk+++K+1+ ++ ++++++
 query 6 YCYLRVVGKGSYGCVTLVKHR-RDGKQYVIKKLN--LRNASSRerrA 49

f1rEiqilkrLshPNivrligvfedtdhlylvmEymegGdlfdylrrng
 + E+q+1 +L+HpnIv+++++e d+ ly+vm ++egGdl++ 1++++
 query 50 AEQEAQLLSQLKHPNIVTYKESWEGDGLLYVMGFCEGDLYRKLKEQK 99

.gp1sekeakkialQilrgleyLHsngivHRDLKpeNIl1dendgtvkia
 + 1+++++ ++ Qi+ +1+YLH+++i+HRDLK++N++1++ + +K++
 query 100 GQLLPENQVWEVFOIAMAALOYLHEKHILHRDLKTQNVFLTRT-NIIRKVG 148

DFGLAr1le.sssklttfvGTpwYmmAPEvilegrgysskVDwS1Gvil
 D G+Ar+le++ +++t+ GTP+Ym +PE+ ++++Y k+DvW+1G+ +
 query 149 DLGIARVLNHCDMASTLIGTPYYM-SPEL-FSNKPYNYKSDVWALGCCV 196

YELLtgpglfpgadlpafgtgdevdq1iifv1klpfsdelpktridplee
 YE+++ k f +d+ +
 query 197 YEMATL-----KHAfNA-----KDMNSL 214

lfriikrpglrlp1psncSeelkdl1kkclnkDpskrpGsatakeilnhpwf<-*
 ++rii++ ++p p+ S+el +L++ +L k P++Rp + + il p++
 query 215 VYRIIEG--KLPMWRDYSPELAELIRTM1LSKRPEERP---SVRSILRQPYI 261

FIGURE 25

Dominant Negative Mutants for Cdc7L1

Point mutant : K90A, D196N - K90A corresponds to a mutation in the catalytic residue in the kinase domain
D196N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

CDC7L1	MEASLGIQMDEPMAFSPQRDRFQAEGSLKXNEQNFKLAVKQDIEKLYEAVPQLSNVFKI
CDC7Sc	-----MTSKTKNIDIPPEIKKEMIQLYHDLPGIENEYKL
	: *.: : . : *.: : *.: : *.: : *.: : *
	○
CDC7L1	EDKIGEGTFSSVYLAT-----AQLQVGPEEKIALKHLIPTSHPIRIAAELQCLT
CDC7Sc	IDKIGEGTFSSVYKAKDITGKITKKFASHFWNGSYVALKKIYVTSSPQRIYNELNLLY
	***** * .: : *.: : *.: : *.: : *
CDC7L1	VAGGQDNVMGVKCYCFRKNHVVIAAMPYLEHESFLDILNSLFQEVREYMLNLFKALKRIH
CDC7Sc	IMTGSSRVAPLCDAKRVRDQVIAPLPYPHEEFRTFRDLPIKGIKKIYIWEILLRALKFVH
	: *... * : . * *.: : * * *.: : *.: : *.: : *
	○
CDC7L1	QFGIVHRDVKPSNFLYNRLKKYALVDFGLAQGTHDTKIELLKVFVQSEAQQERCSONKSH
CDC7Sc	SKGI.IHRDIKPTNLFNLELGRGVLVDFGLAEAQMDYKSMISSQND-----
	. **.: **.: **.: * .: . *****.: * * : . :
CDC7L1	IITGNKIPLSGVPVKELDQQSTTKASVKRPTYTNAQIQKQKDGKESVGLSVQRSVFGE
CDC7Sc	-----YDN-----YANTNHDGGYSMRNHEQFCPC
	: . .: . *.: : *.: : *
CDC7L1	RNFNIHSSISHESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASL
CDC7Sc	IMRNQYSPNSHNQTPPMVTIQNGKVHLN-----
	* :*. **.:... : *. * *
CDC7L1	TCDCYATDKVCSICLSRRQVAPRAGTGFRAPEVLTCPNQTTAIDMWSAGVIFLSLLS
CDC7Sc	NVANGVDLTGKYPKNETRRIKRANRAGTRGFRAPVLKMGCAQSTKIDISVGVILLSLLG
	. : * . . : ** : * **** ***** ** *.: **.: **.: **.: **.: *

FIGURE 26

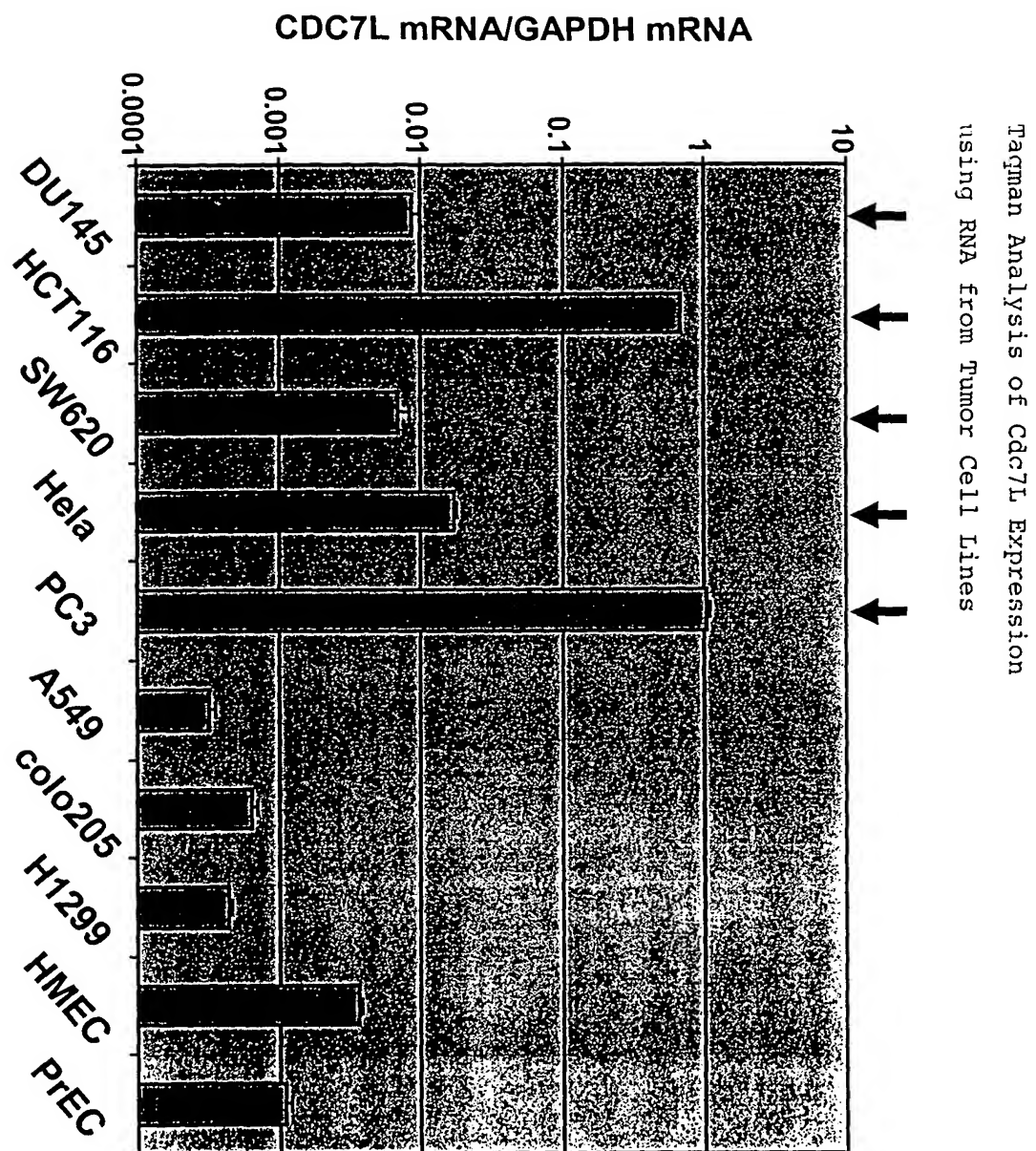


FIGURE 27

CDC7L mRNA Levels are Higher in Diseased Tissue
 Relative to Normal Tissue in Patients with Lung Carcinomas

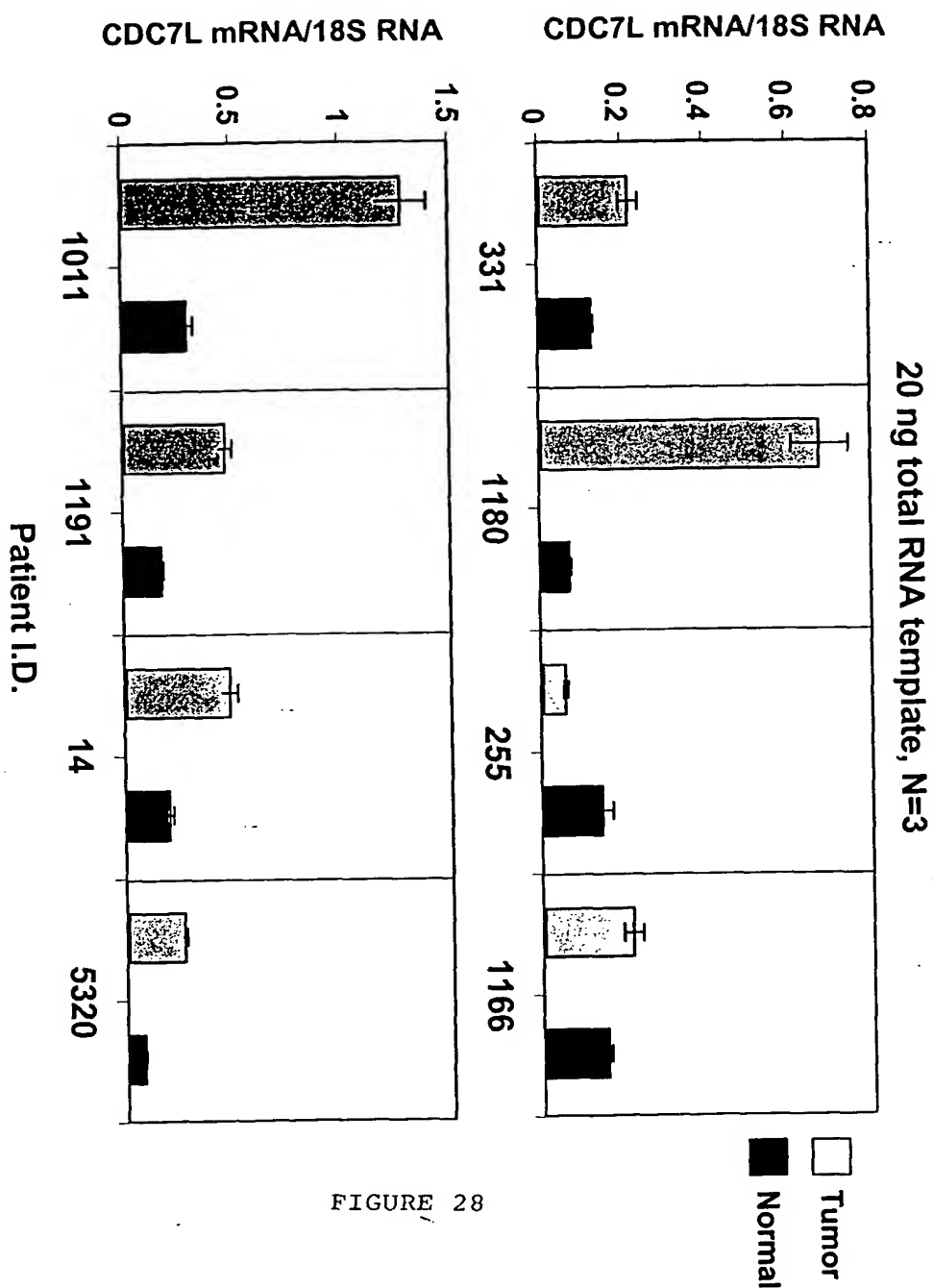


FIGURE 28

CDC7L mRNA Levels are Higher in Diseased Tissue
Relative to Normal Tissue in Patients with Colon Carcinoma

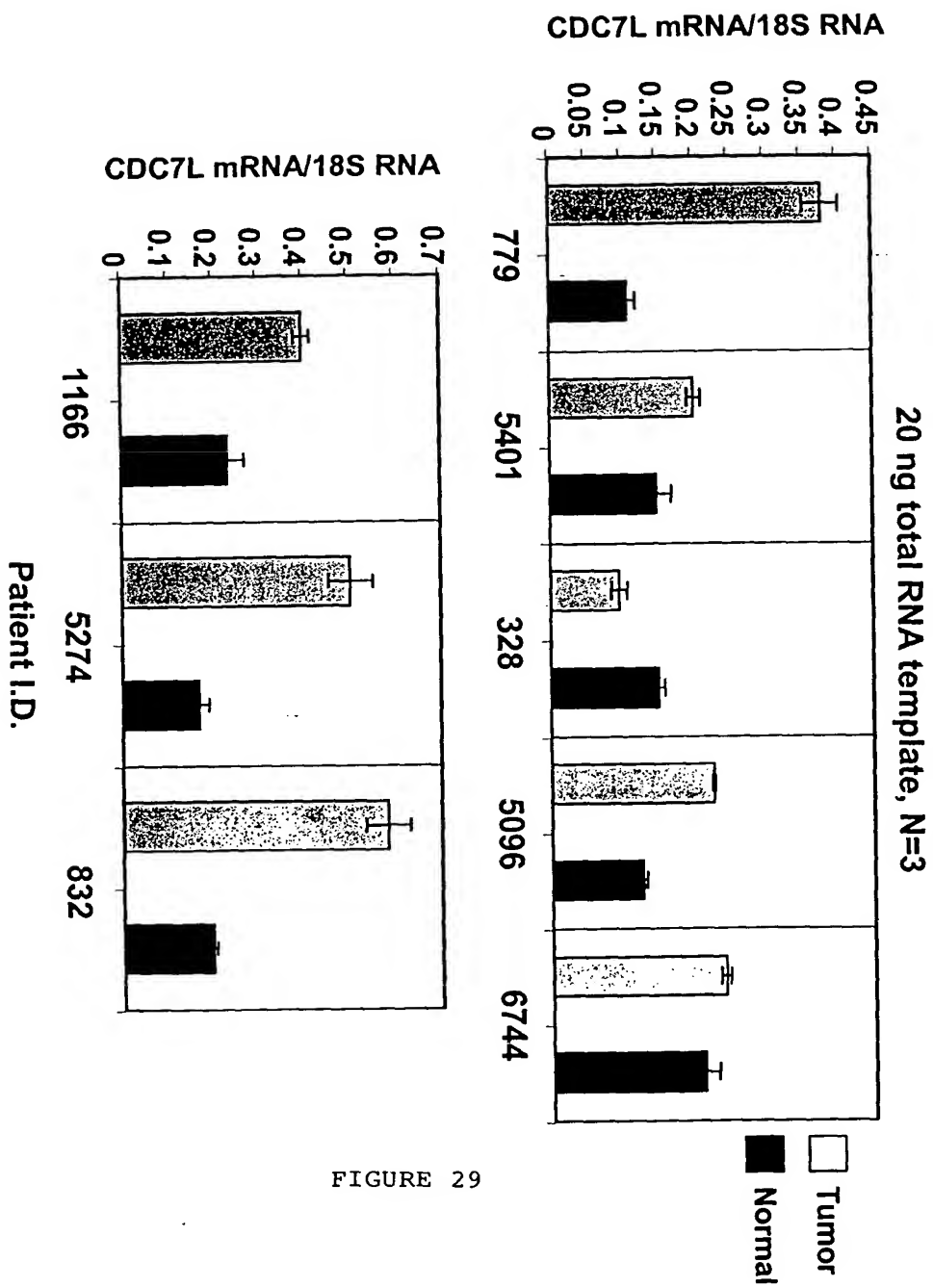


FIGURE 29

Taqman Analysis of CNK Expression Using RNA from Tumor Cell Lines

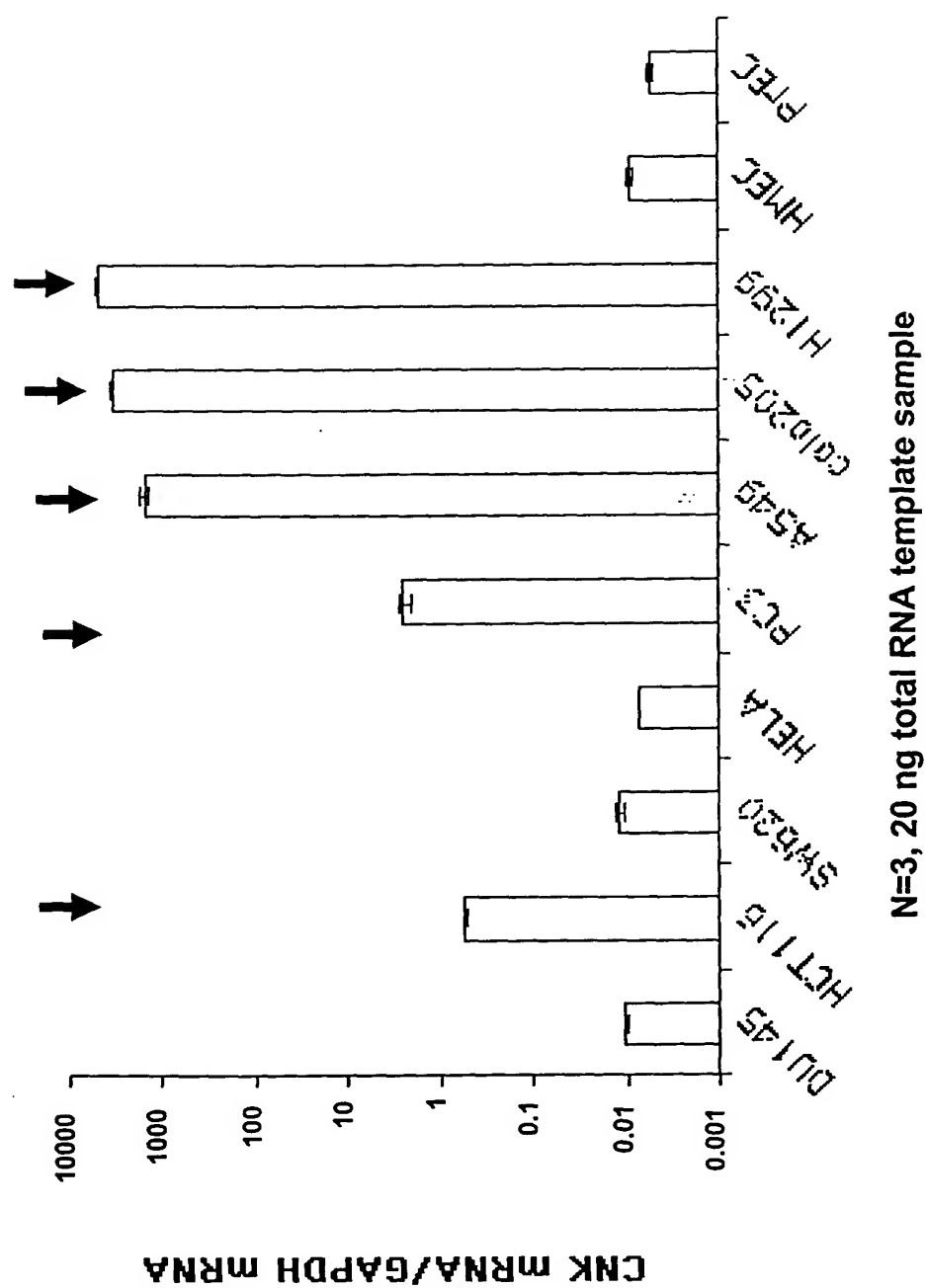


FIGURE 30

13



Kinase reactions were performed for 30 minutes at R.T. using 2 clones of each construct.

RT-PCR of mRNAs From Different Tissues and Cell Lines Suggests that the Larger STK2 Isoform Predominates in *H. Sapiens*

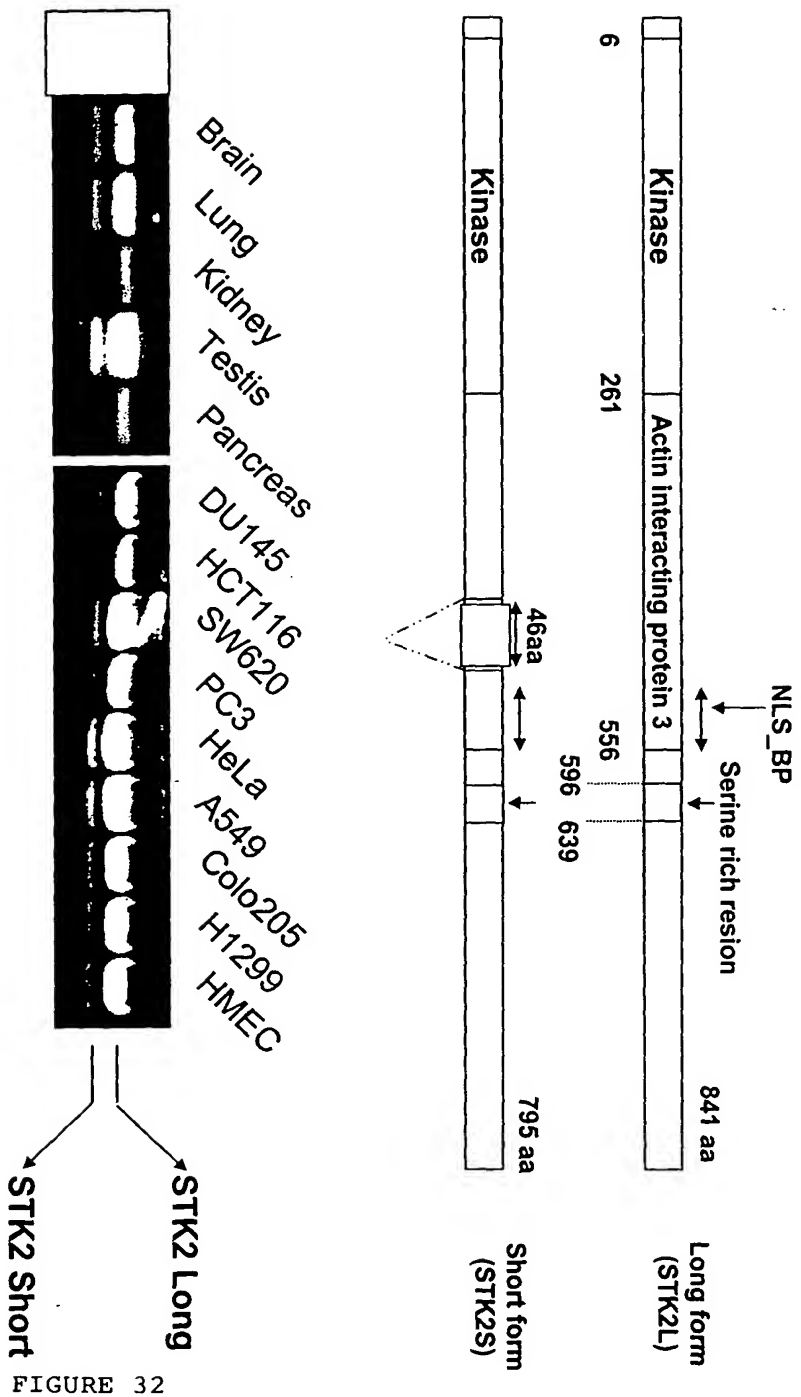
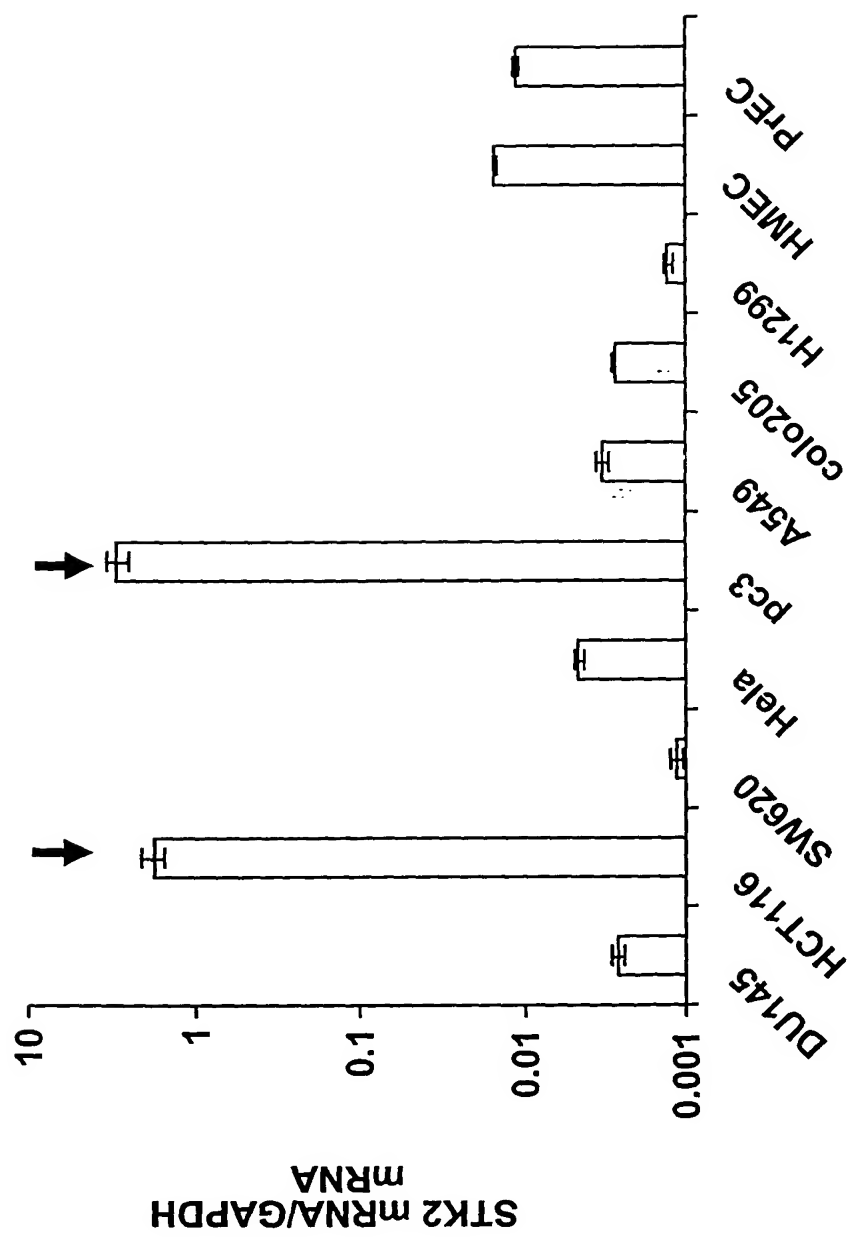


FIGURE 32

Taqman Analysis of STK2 Expression using RNA from Tumor Cell Lines



N=3, 20 ng total RNA template sample

FIGURE 33

GFP-STK2 Short is Antiproliferative when Measured Using the Cell Tracker Assay

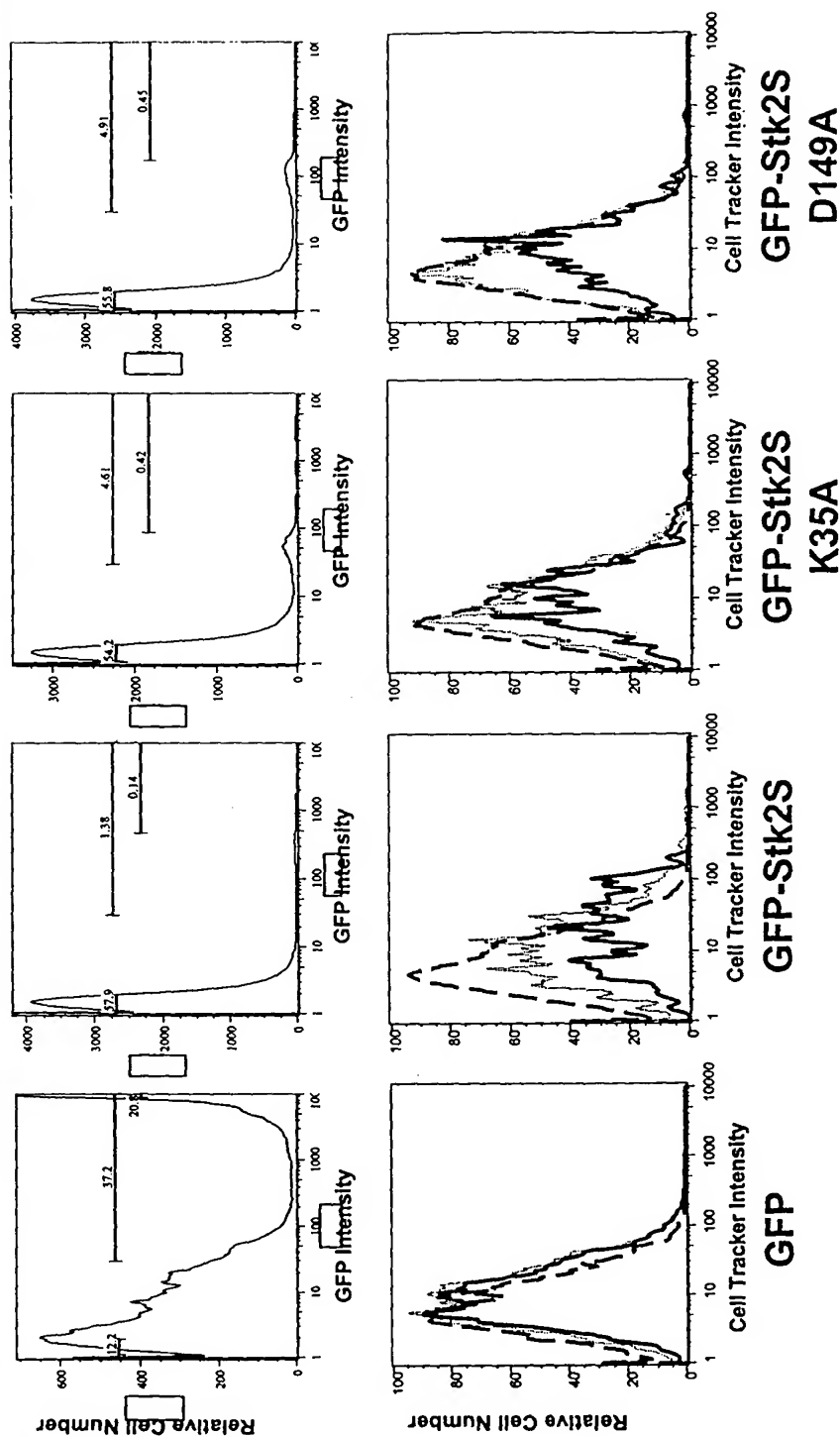


FIGURE 34

Cell Tracker Assay Day 8 A549 GFP Pos. --- GFP Neg. — GFP Hi

Expression of GFP-Stk2 Long is Antiproliferative in A549 and HeLa Cells

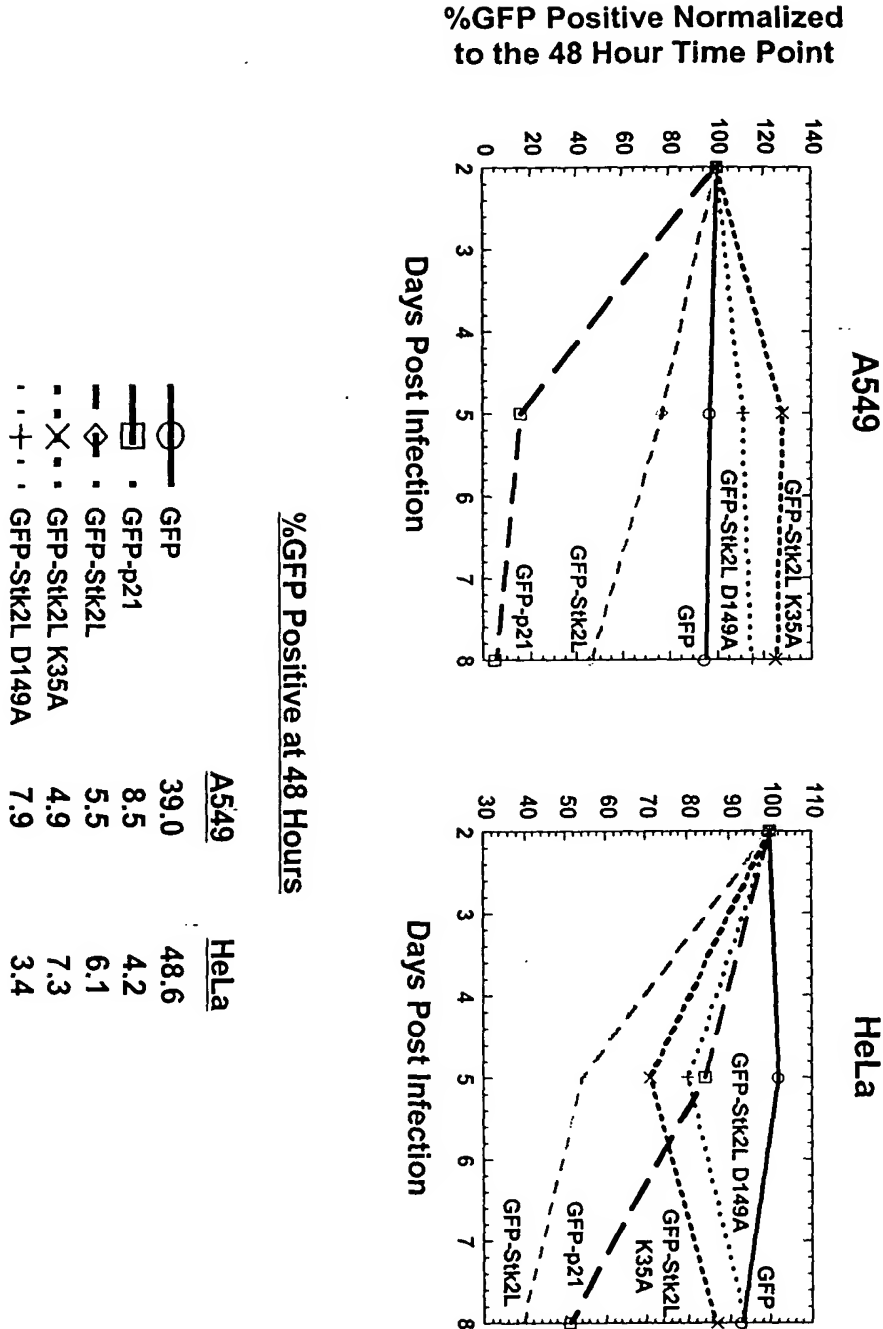


FIGURE 35

GFP-STK2 Long is Antiproliferative when Measured Using the Cell Tracker Assay

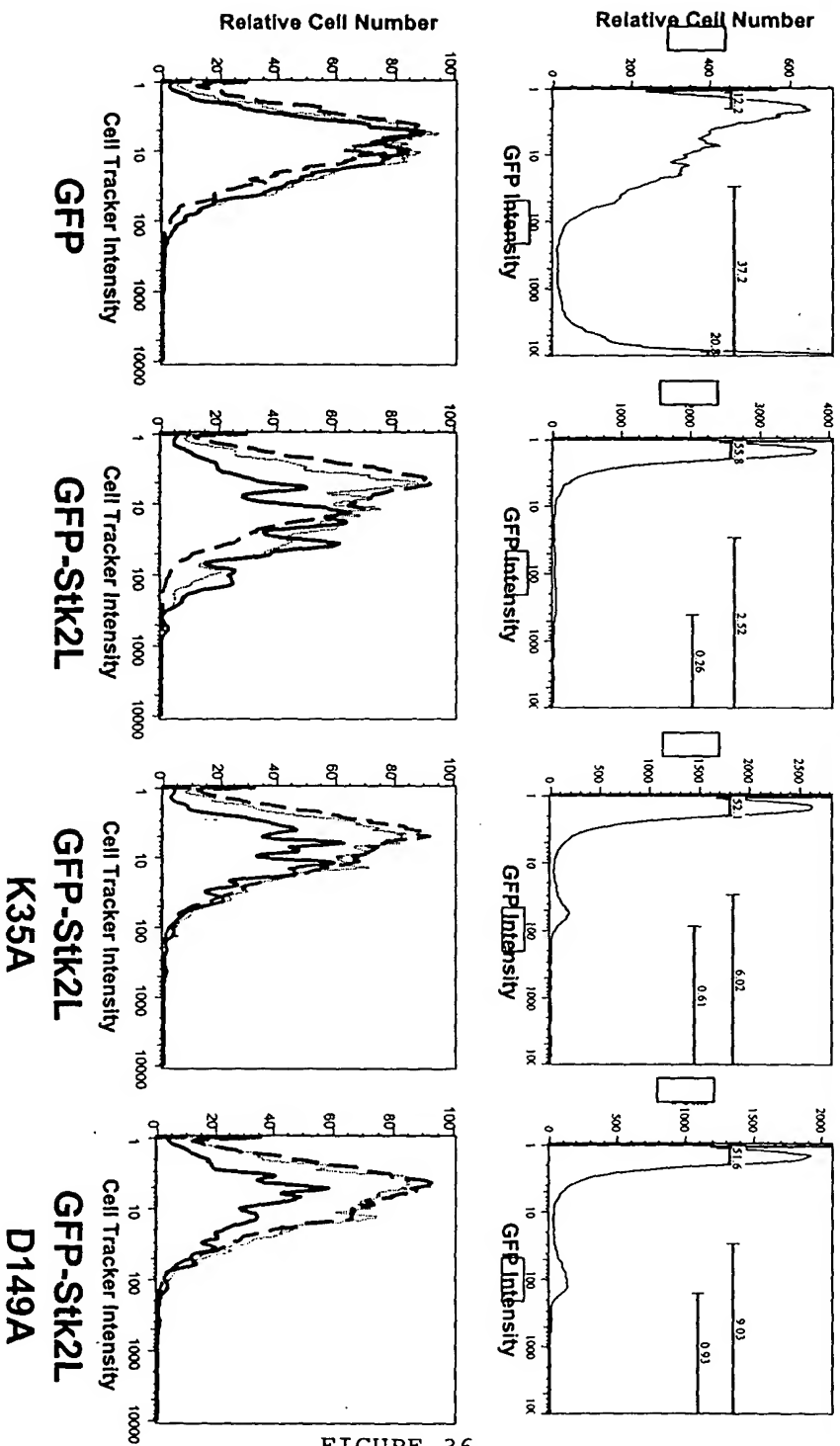


FIGURE 36

Cell Tracker Assay Day 8 A549 GFP Pos. — GFP Neg. — GFP Hi

Expression of STK2L WT and Mutants Using IRES Vectors is Antiproliferative in A549 Cells

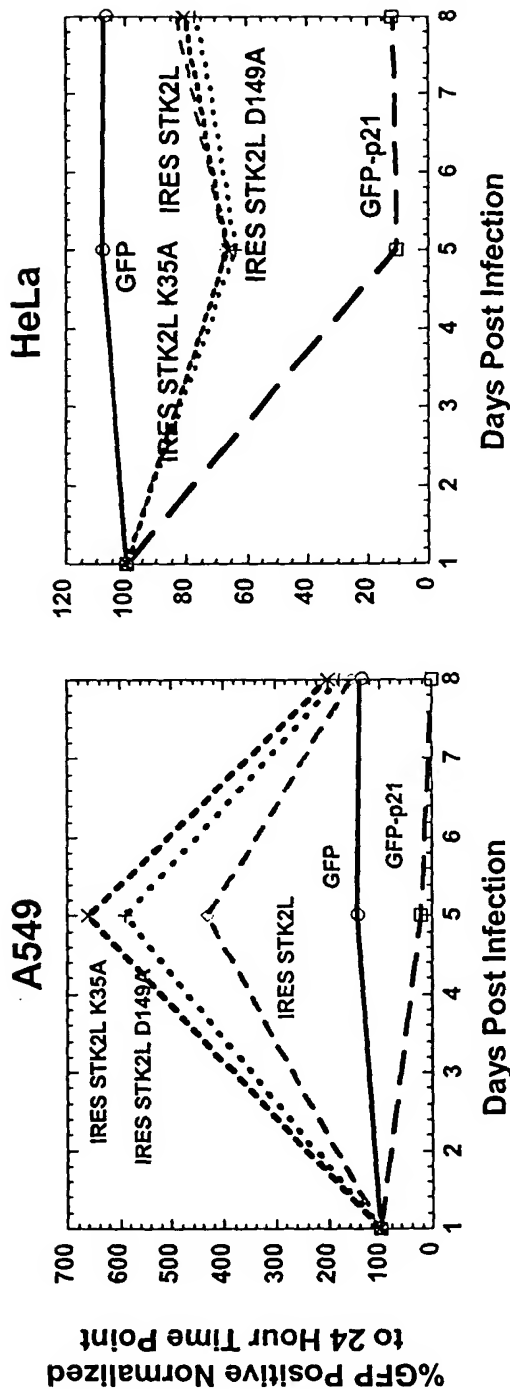


FIGURE 37

%GFP Positive at 24 Hours		A549	HeLa
	GFP	52.8	59.0
	GFP-p21	11.0	23.1
	IRES STK2L	0.80	0.64
	IRES STK2L K35A	1.79	2.3
	IRES STK2L D149A	1.93	4.4

IRES Hbo1 E508Q is Antiproliferative in A549 Cells

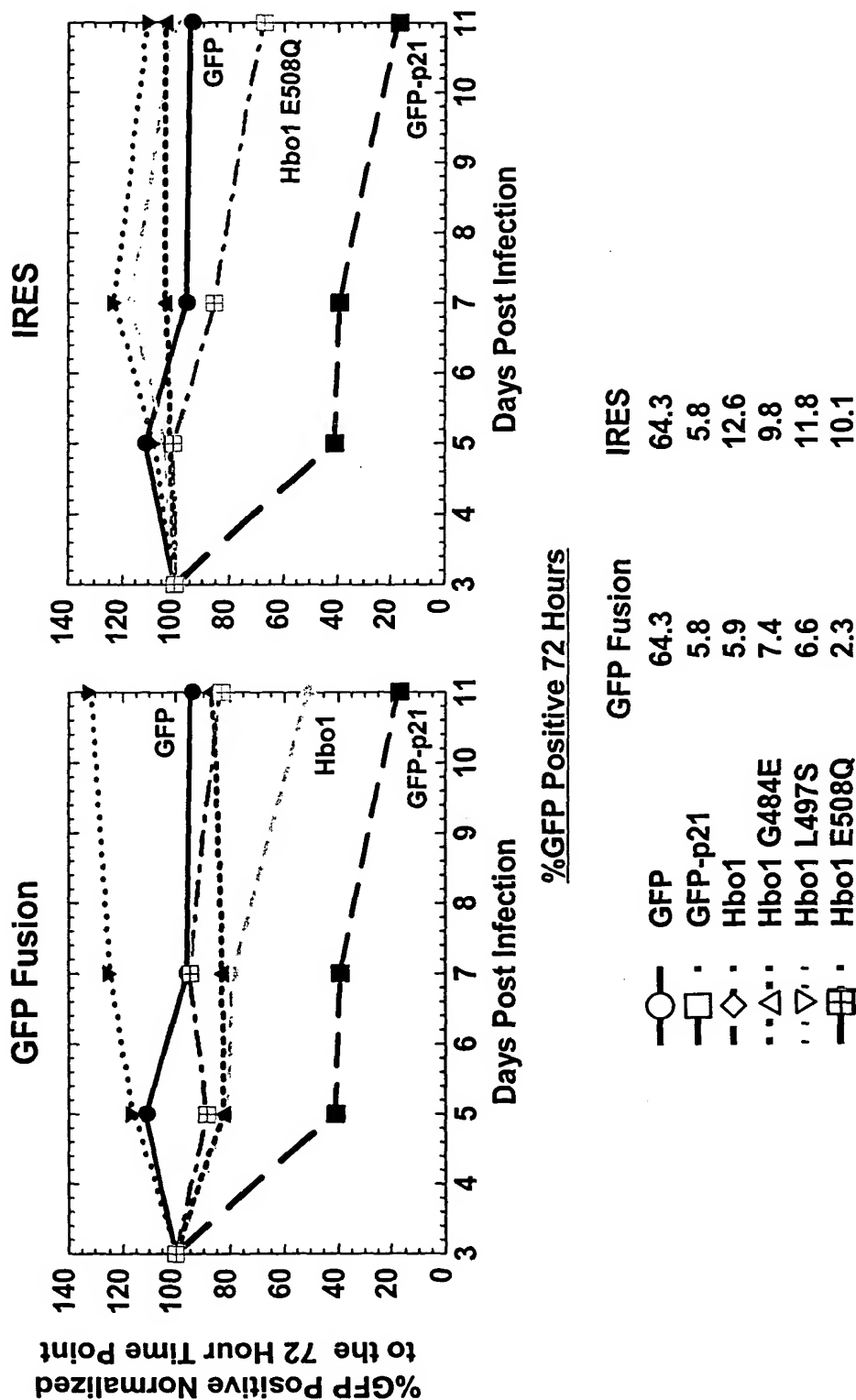


FIGURE 38

GFP-Hbo1 has a dominant negative effect which is not observed with the IRES construct

No Significant Differences are Observed Between Hbo1 WT and Mutant Proteins in H1299 Cells

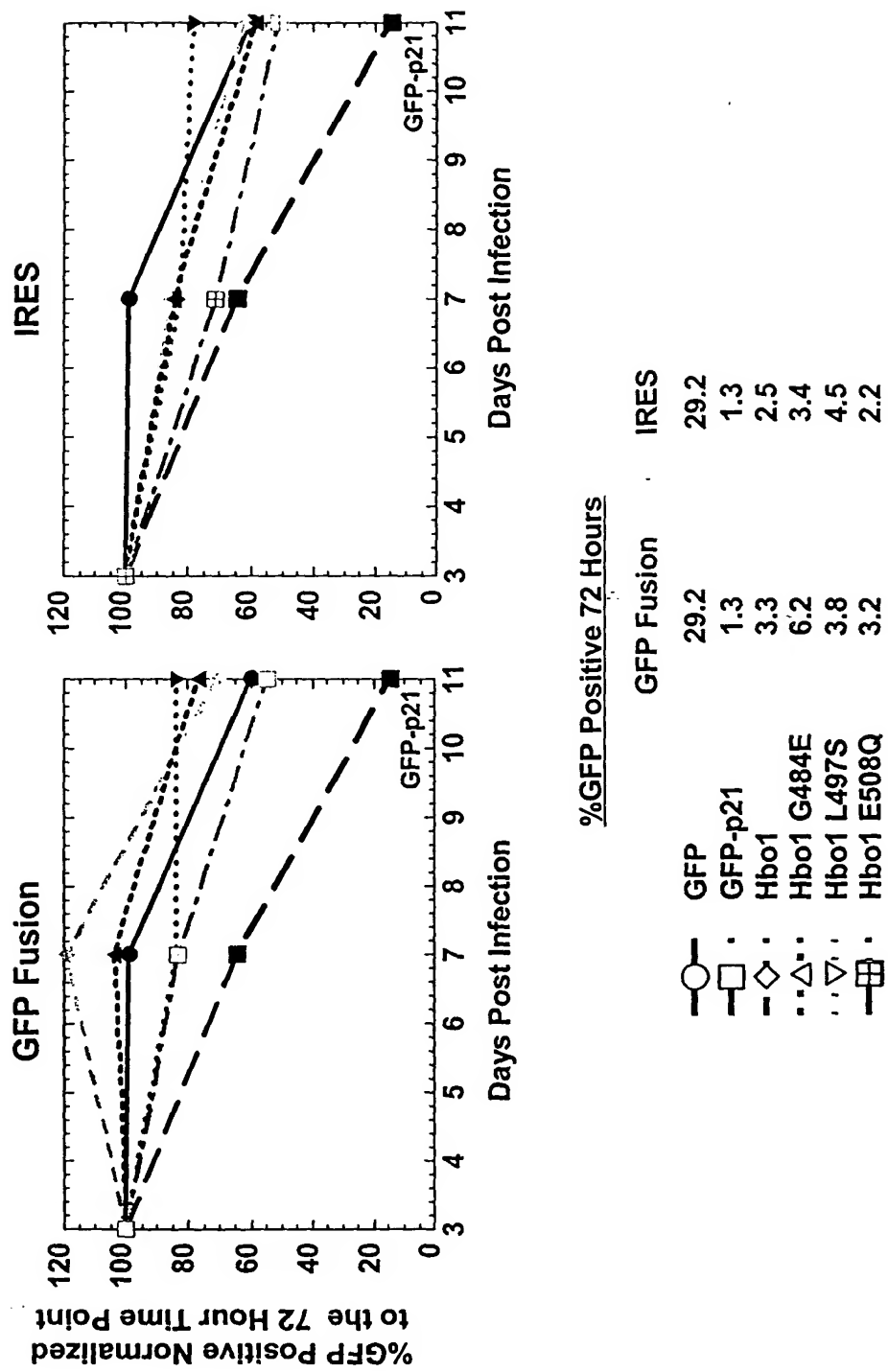
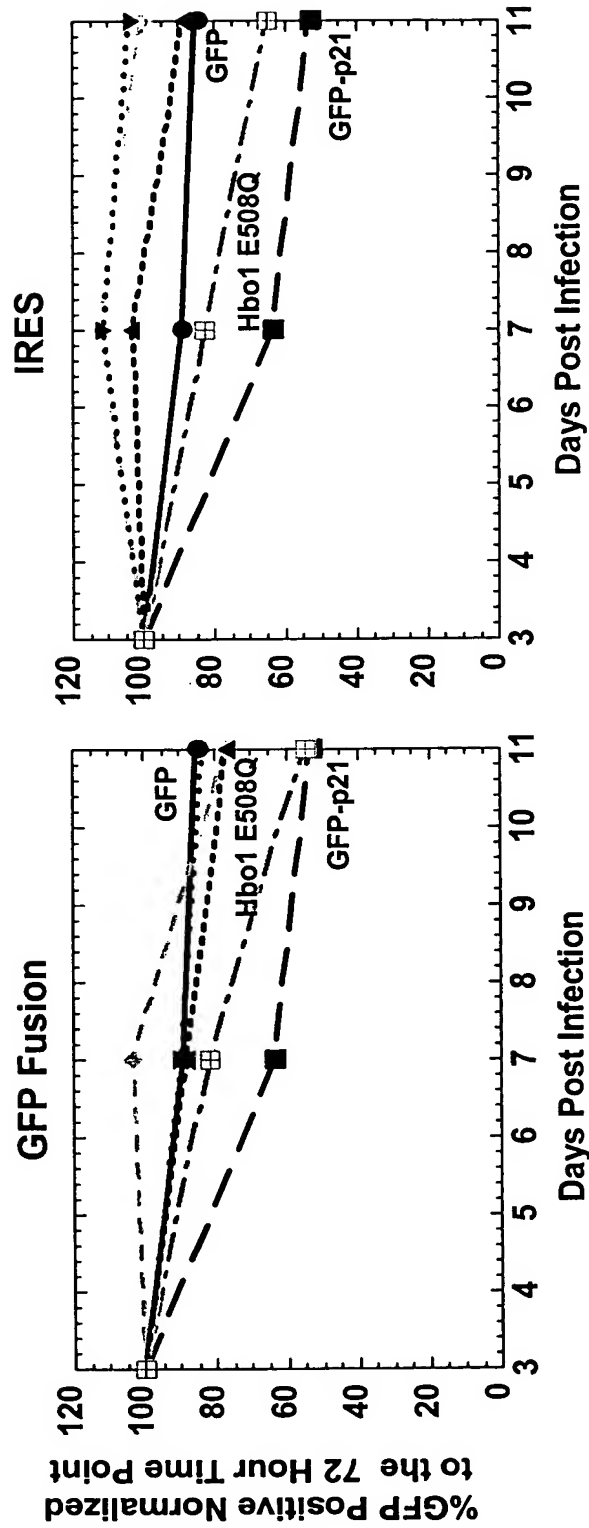


FIGURE 39

Hbo1 E508Q is Antiproliferative in HeLa Cells



%GFP Positive 72 Hours

	GFP Fusion	IRES
GFP	100	100
GFP-p21	15.8	15.8
Hbo1	10.7	9.3
Hbo1 G484E	17.1	11.4
Hbo1 L497S	11.8	17.7
Hbo1 E508Q	10.2	5.2

FIGURE 40

Analyzing proliferation of Sorted Cells Expressing
HRO1 WT or Dominant Negative Mutants

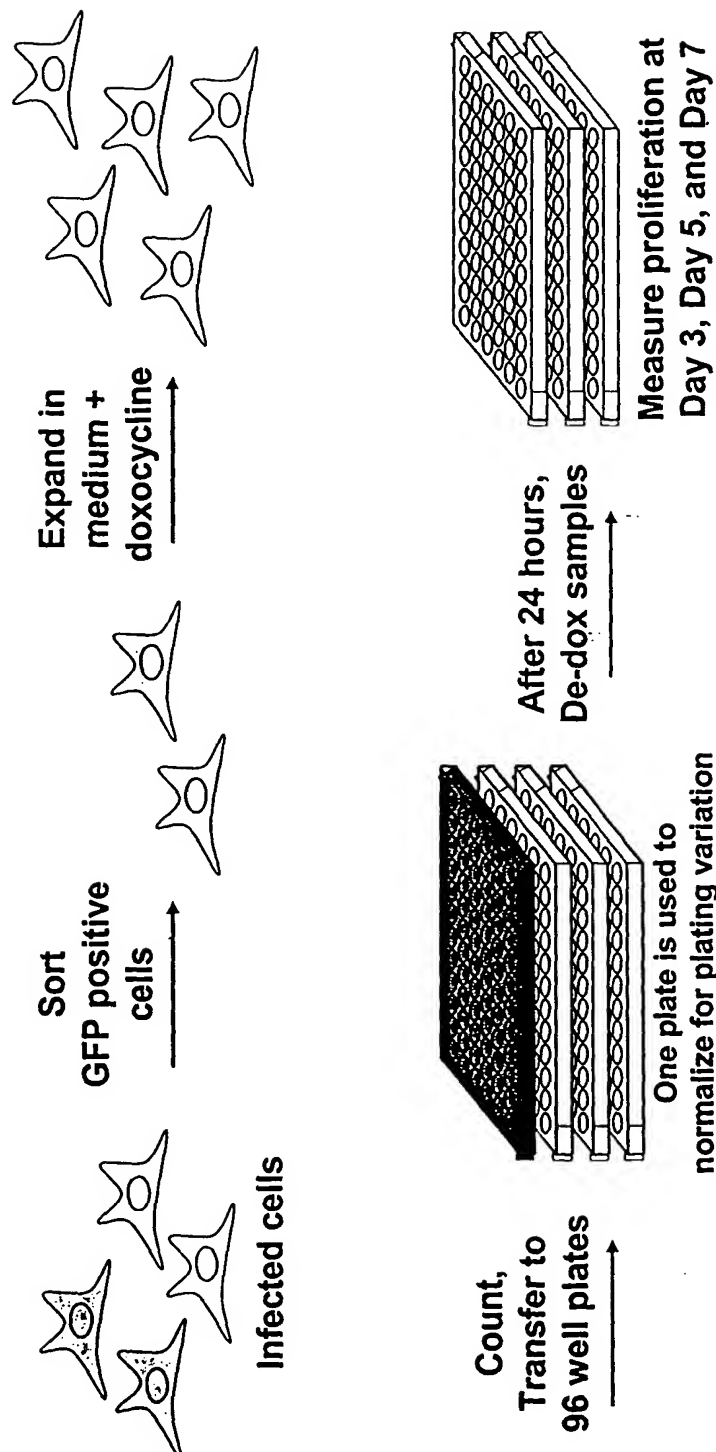


FIGURE 41

Proliferation is measured using the CyQuant Cell Proliferation Assay (Molecular Probes) which is based upon the fluorescence enhancement upon binding of a proprietary dye to cellular DNA

HBO1 E508Q is Antiproliferative in A549 Cells

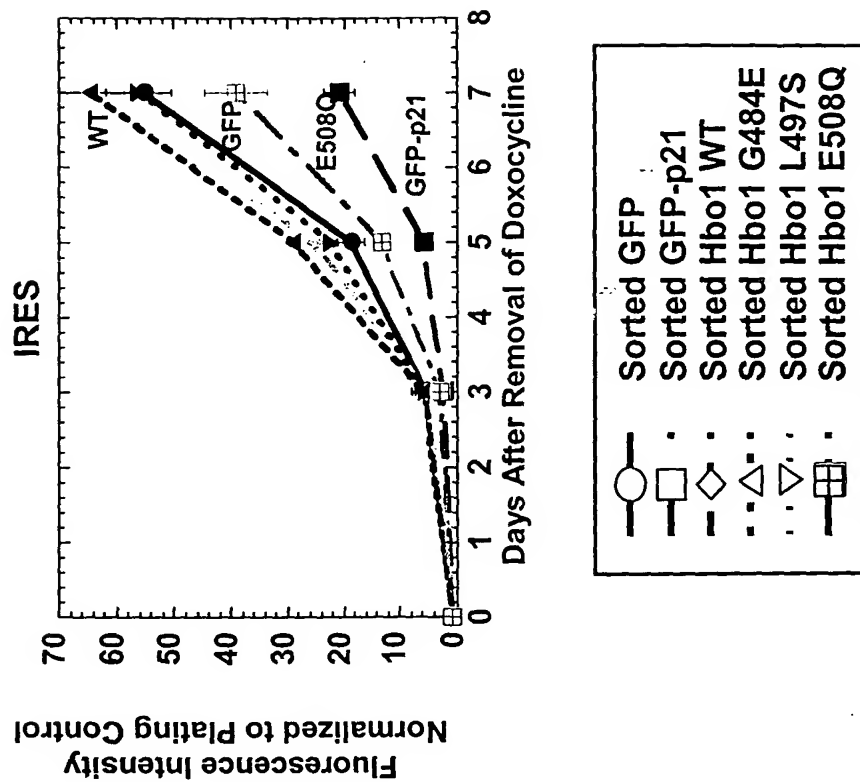


FIGURE 42

HBO1 E508Q is Antiproliferative in HeLa Cells

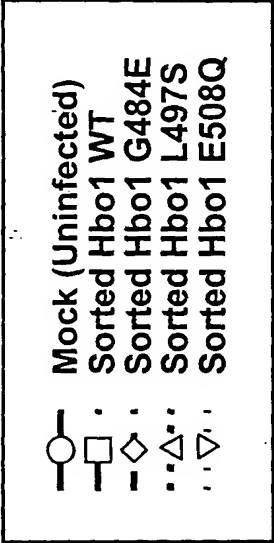
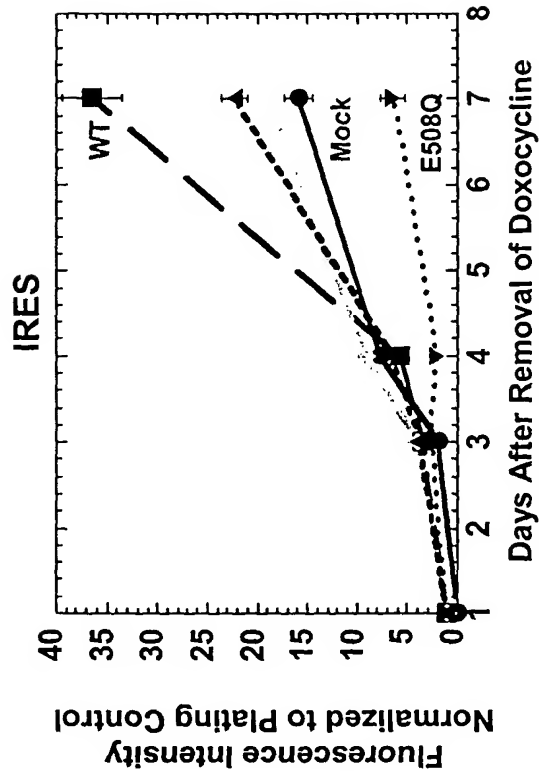


FIGURE 43

HBO1-Specific siRNA Has an Antiproliferative Effect on A549 Cells

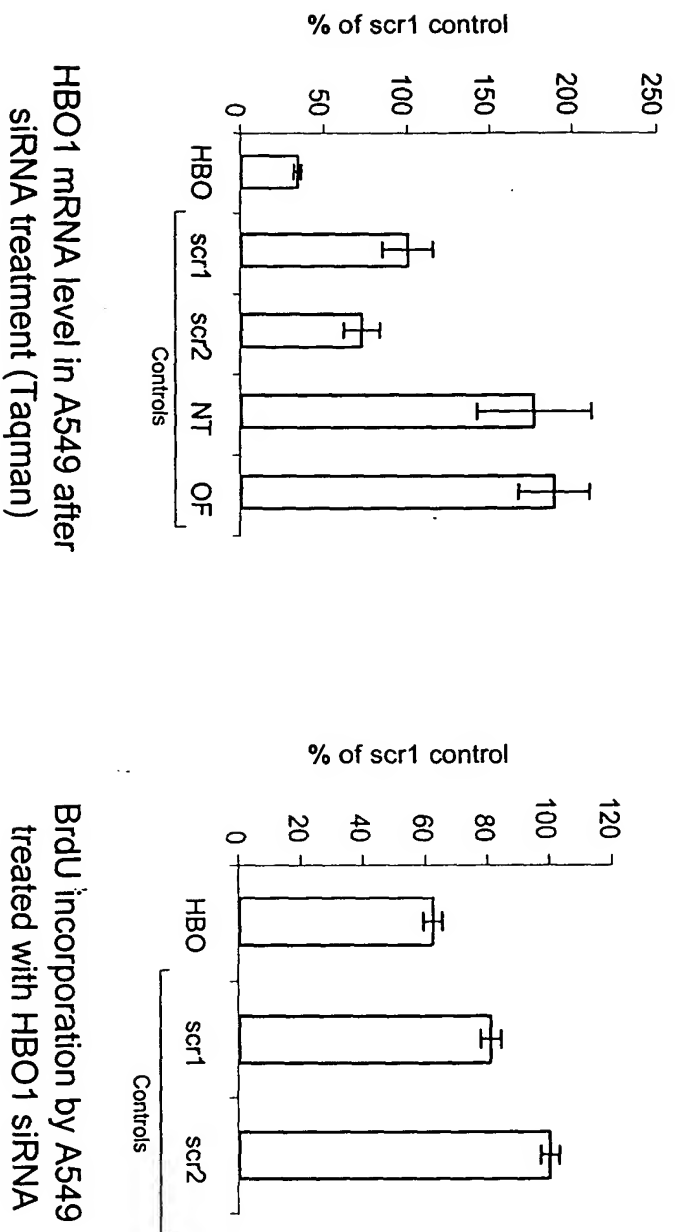


FIGURE 44

HBO1-Specific siRNA Has an Antiproliferative Effect on H1299 Cells

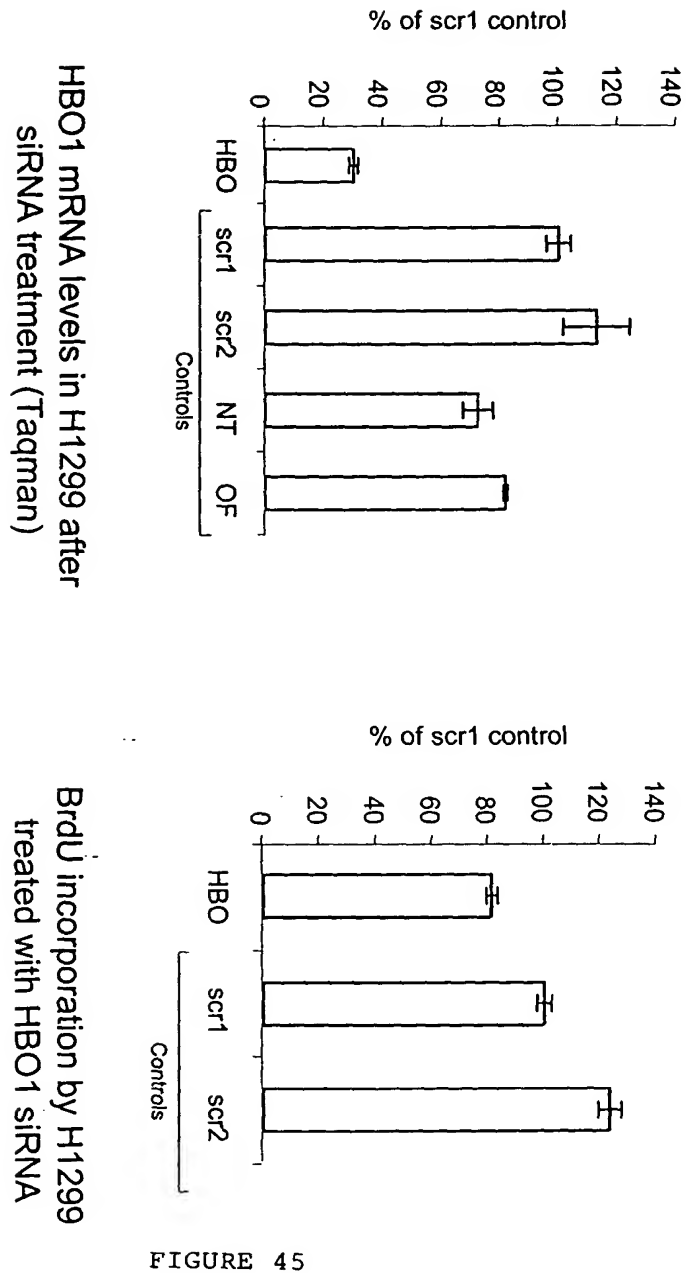


FIGURE 45

Taqman Analysis of PIM-1 Expression Using RNA
from Tumor Cell Lines

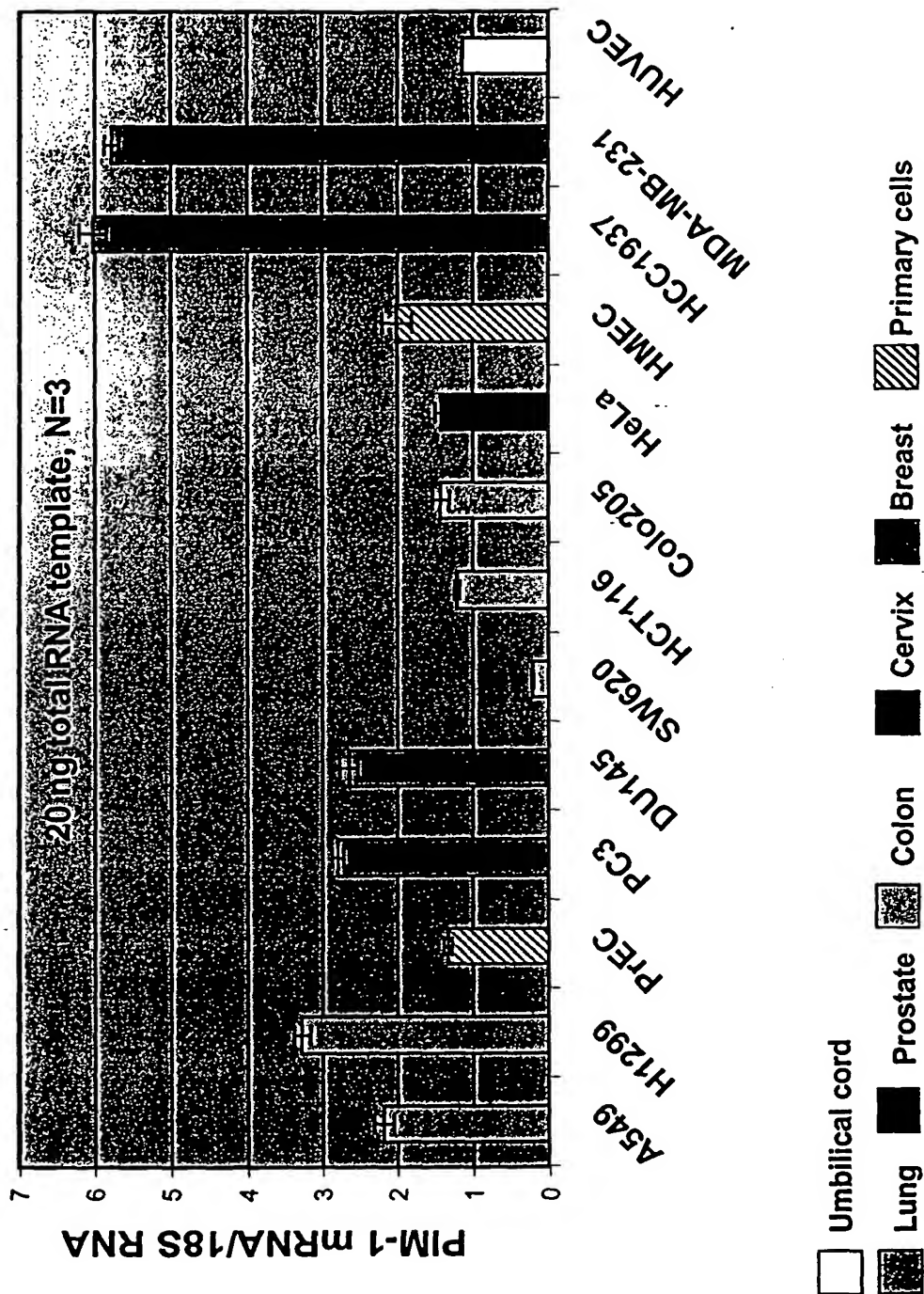


FIGURE 46

Taqman Analysis of PIM-1 mRNA Expression
in Samples Obtained from Patients with Breast Carcinoma

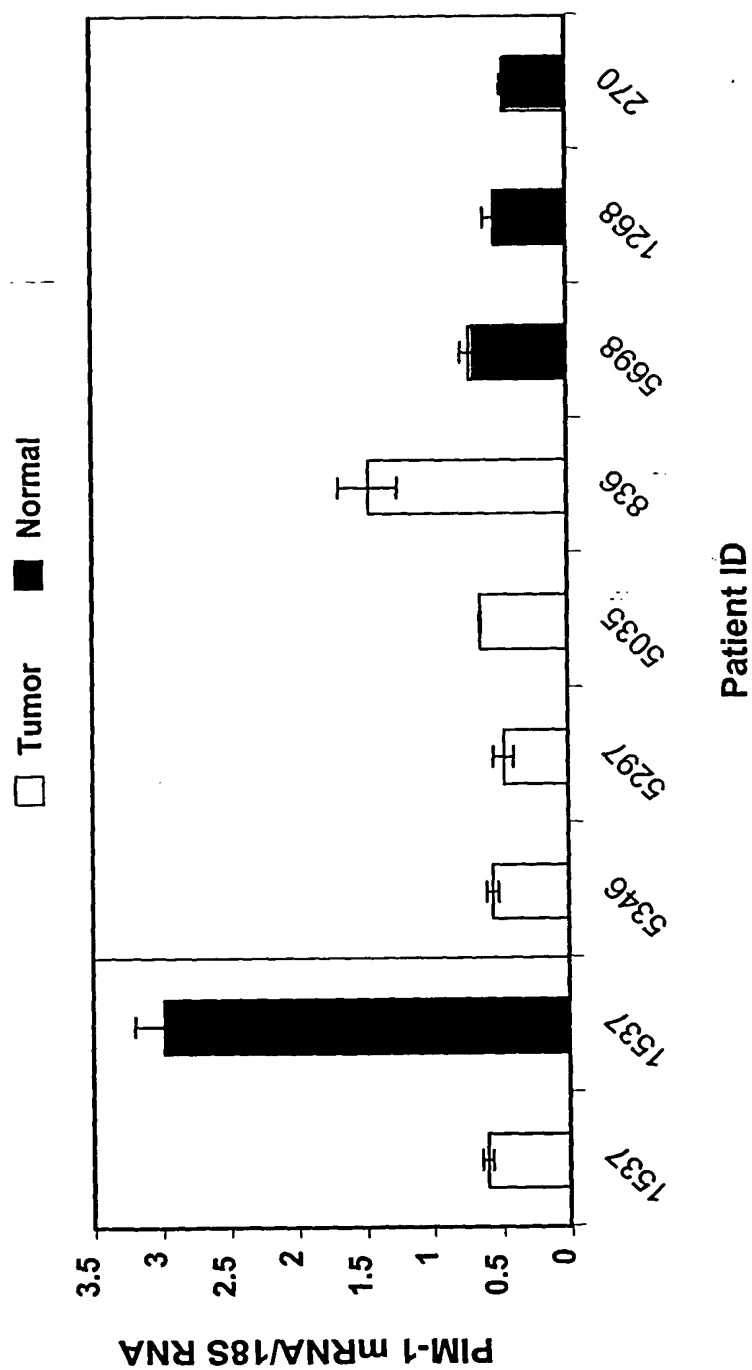


FIGURE 47

N = 3, 20 ng total RNA/sample

Tagman Analysis of PIM-1 mRNA Expression in Samples
 Obtained from Patients with Lung Carcinoma

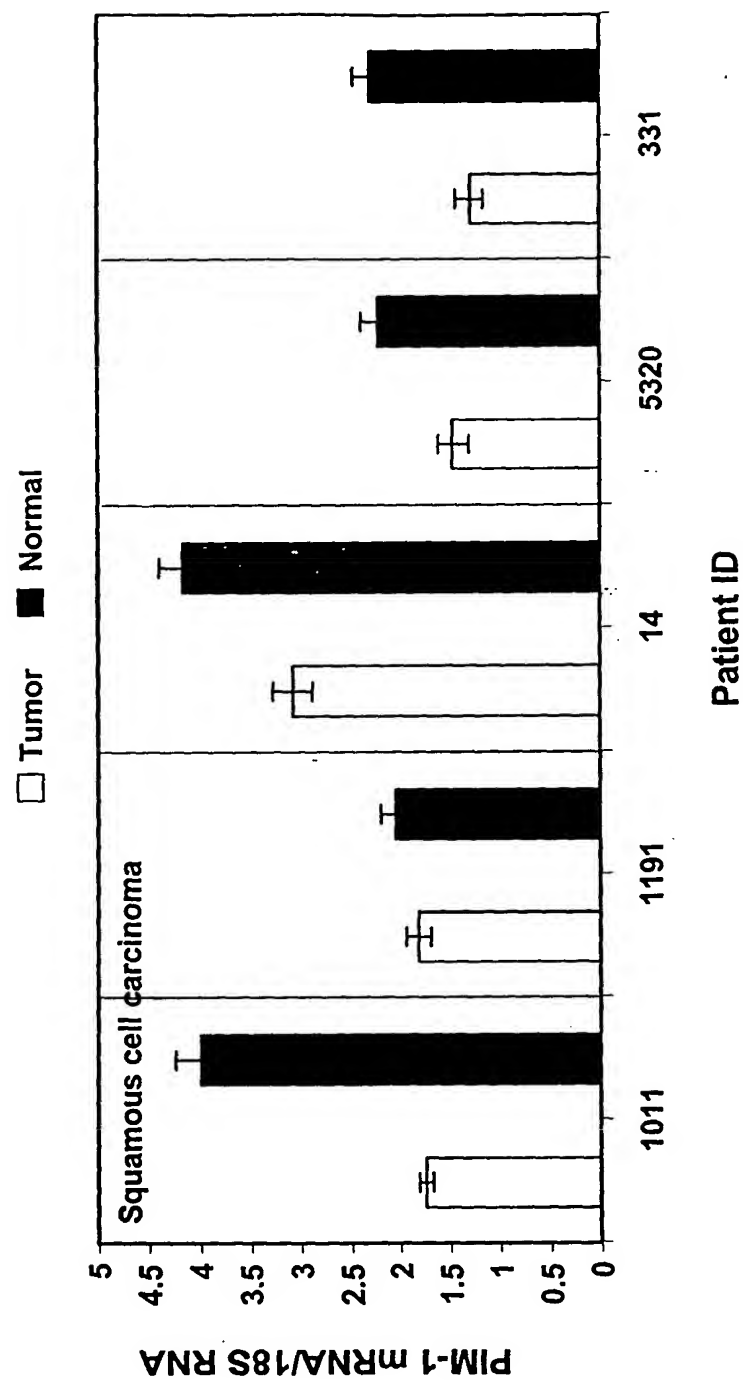


FIGURE 48

N = 3, 20 ng total RNA/sample

%GFP Positive Normalized to the 72 Hour Time Point

GFP Fusion

Days Post Infection	GFP	GFP-p21	Pim-1
3	100	100	100
4	100	100	100
5	100	100	100
6	100	100	100
7	100	100	100
8	100	100	100
9	100	100	100
10	100	100	100

IRES

Days Post Infection	GFP	GFP-p21	Pim-1
3	100	100	100
4	100	100	100
5	100	100	100
6	100	100	100
7	100	100	100
8	100	100	100
9	100	100	100
10	100	100	100

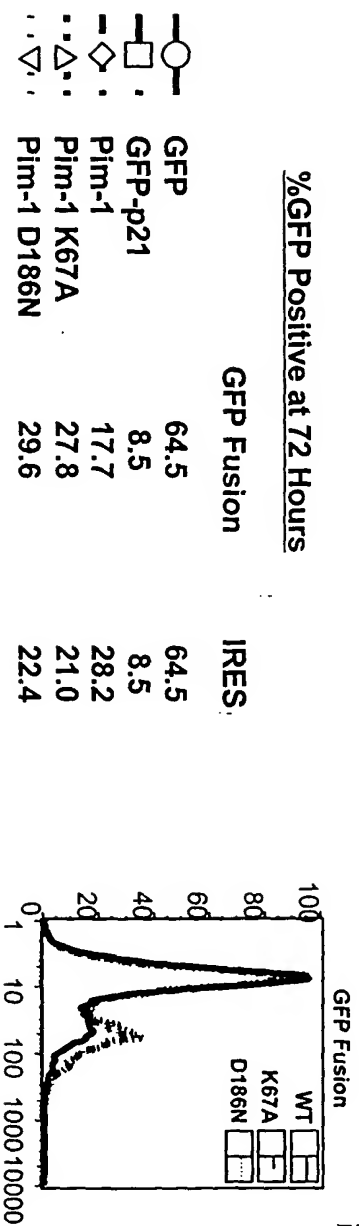


FIGURE 49

In H1299 Cells, Expression of GFP-Pim-1 WT and all IRES constructs is Antiproliferative

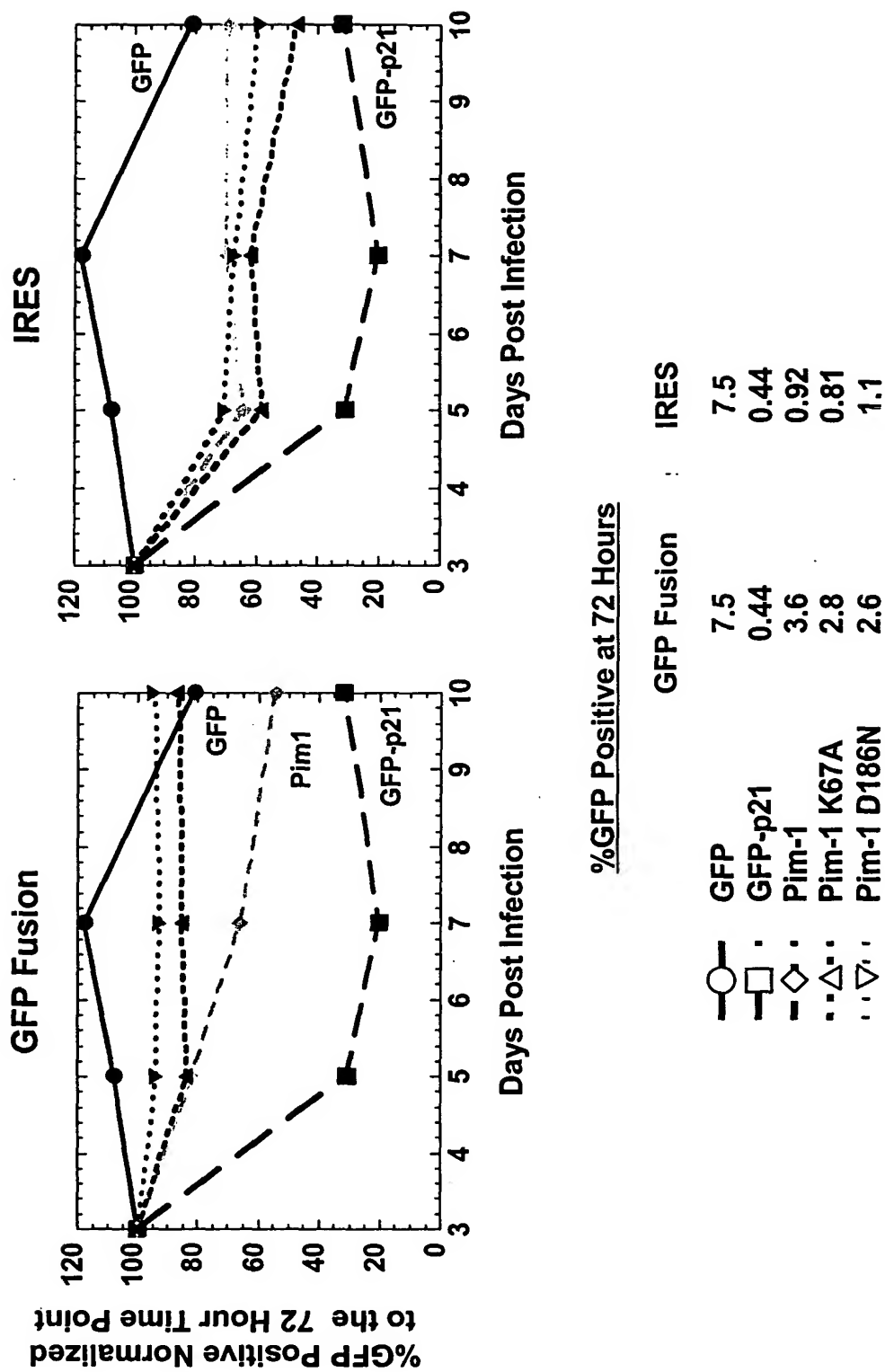


FIGURE 50

PIM-1-Specific siRNA Has an Antiproliferative Effect on A549 Cells



FIGURE 51

PIM-1 mRNA level in A549 after siRNA treatment (Taqman)

BrdU incorporation by A549 treated with PIM-1 siRNA

OF: oligofectamine, NT: no transfection

PIM-1-Specific siRNA Has an Antiproliferative Effect on HeLa Cells

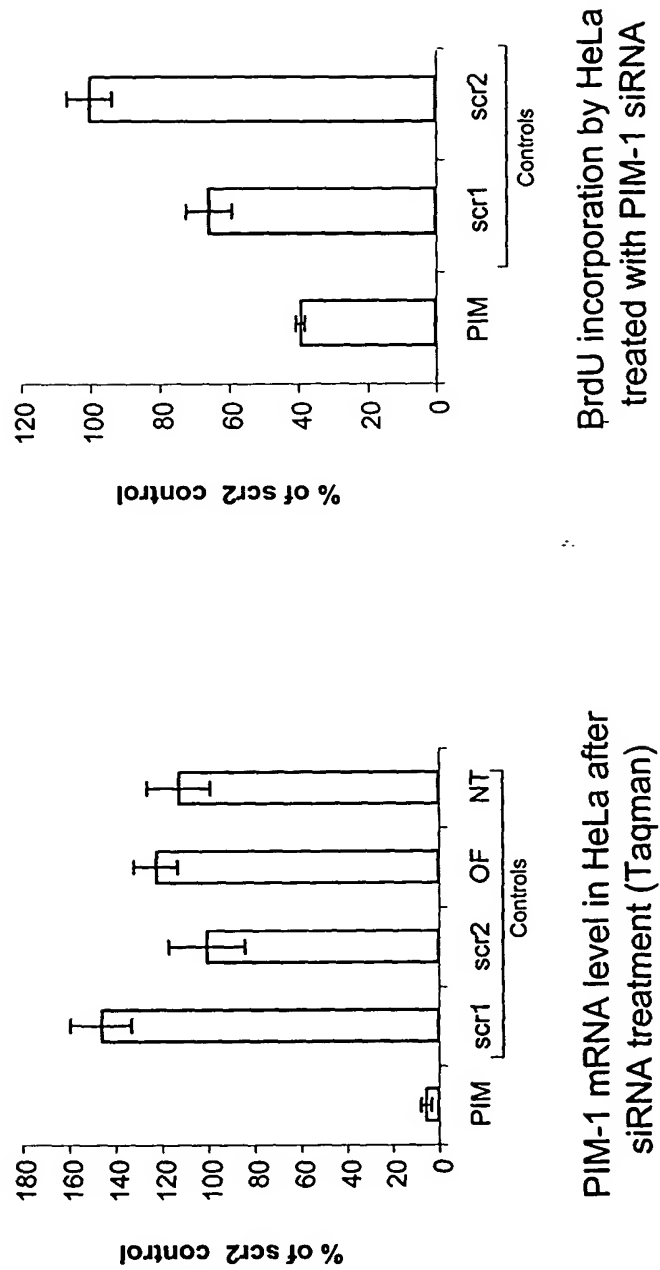
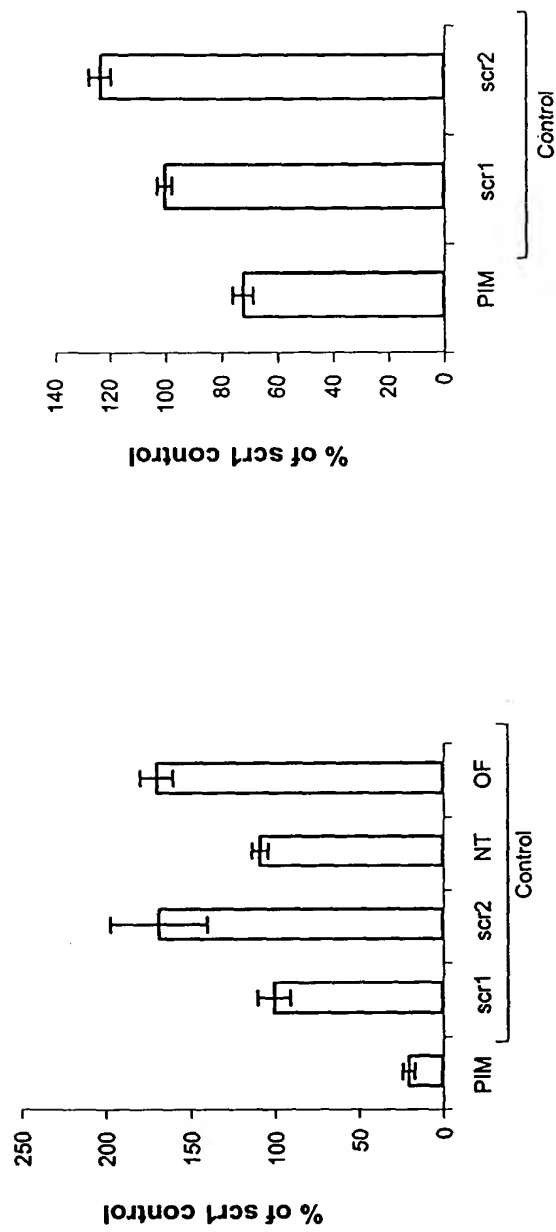


FIGURE 52

OF: oligofectamine, NT: no transfection

PIM-1-Specific siRNA Has an Antiproliferative Effect on H1299 Cells



BrdU incorporation by H1299 treated with PIM-1 siRNA

PIM-1 mRNA level in H1299 after siRNA treatment (Taqman)

OF: oligofectamine, NT: no transfection

FIGURE 53

PIM-1-Specific siRNA Has an Antiproliferative Effect on HUVEC Cells

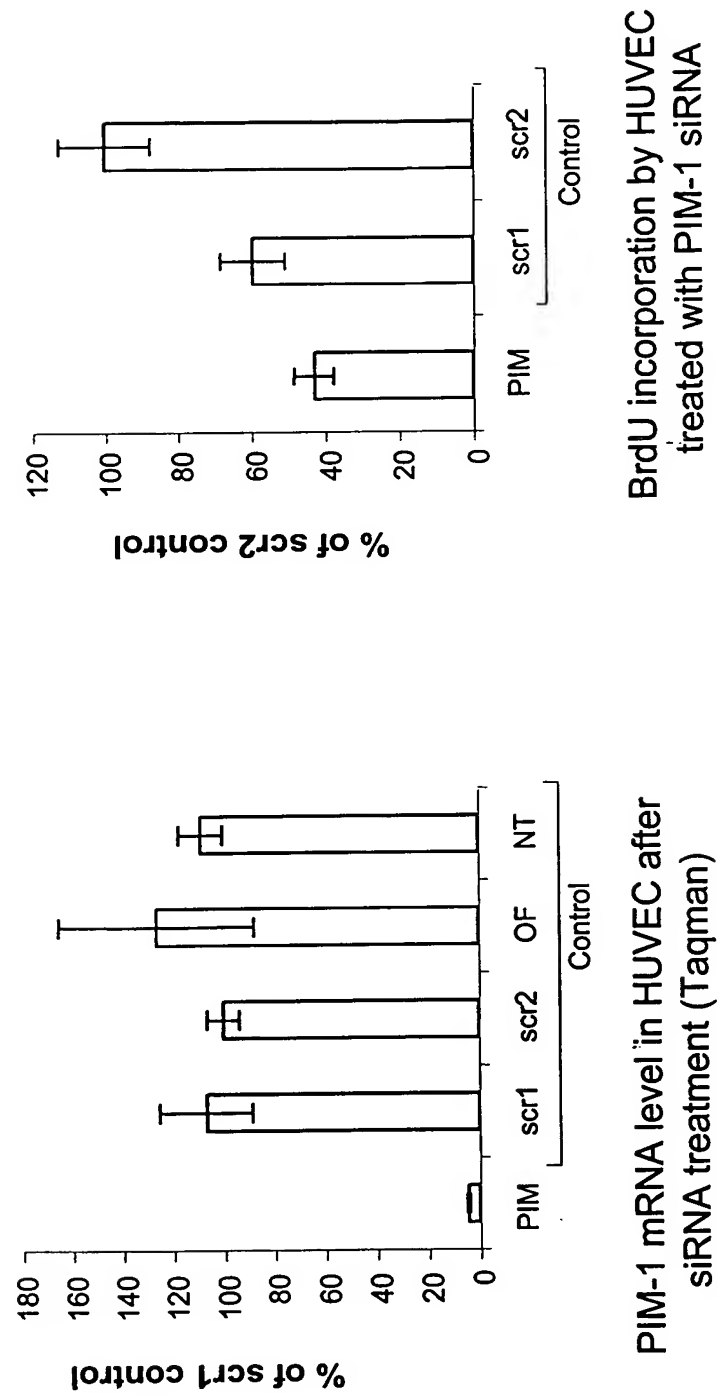
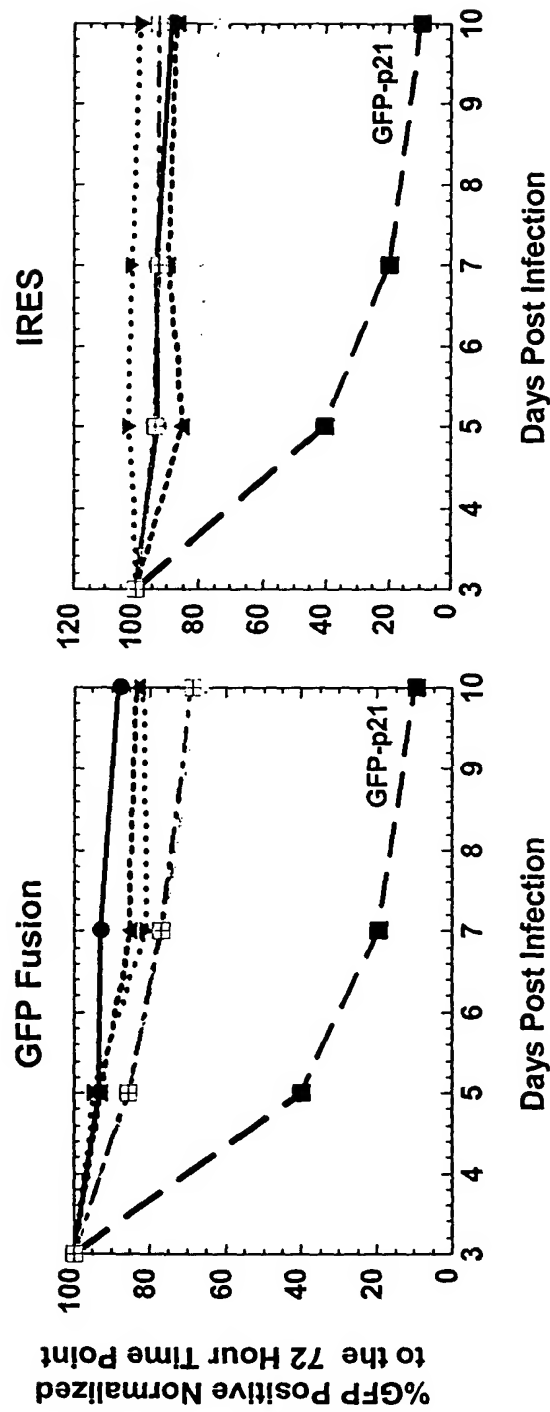


FIGURE 54

OF: oligofectamine, NT: no transfection

No Antiproliferative Effects are Observed for Ape1 WT and Dominant Negative Mutants in A549 Cells

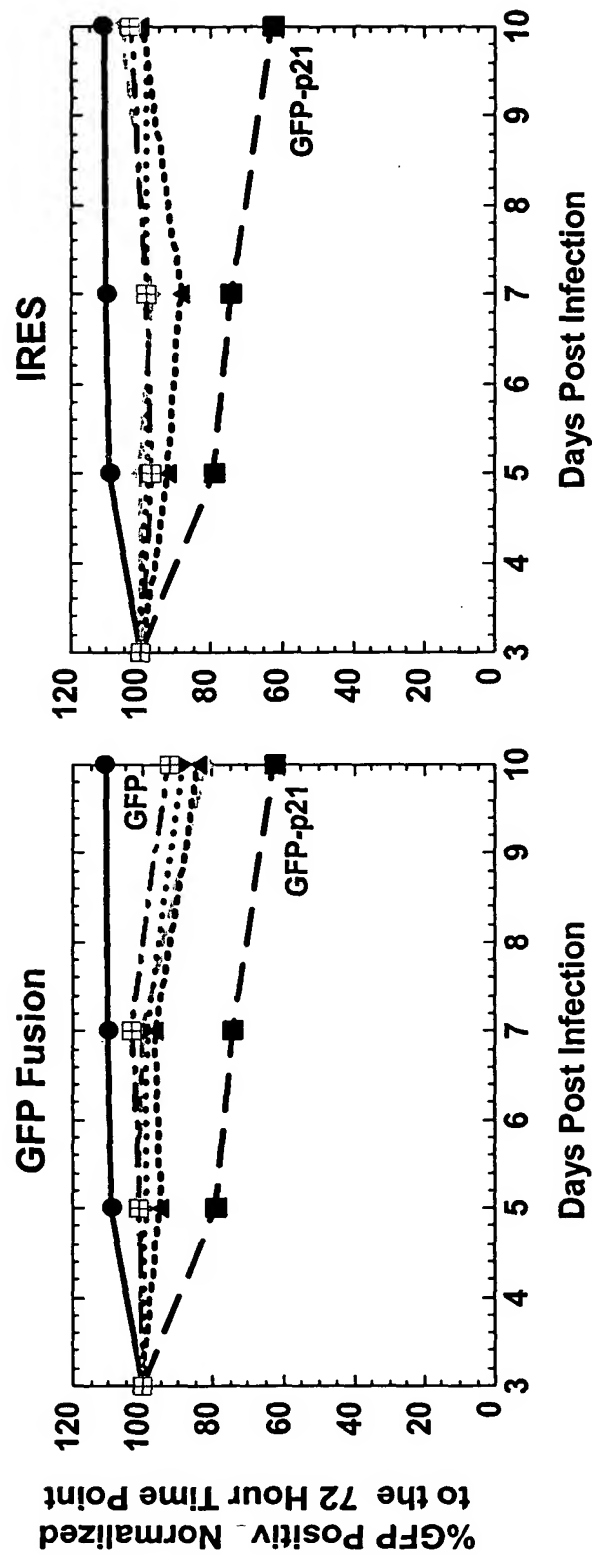


%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	66.4	66.4
GFP-p21	13.2	13.2
Ape1	13.2	13.6
Ape1 E96A	12.9	16.7
Ape1 D210A	14.3	11.3
Ape1 C65A	14.6	17.2

FIGURE 55

GFP-Ape1 WT and Dominant Negative Mutants Have No Effect in H1299 Cells

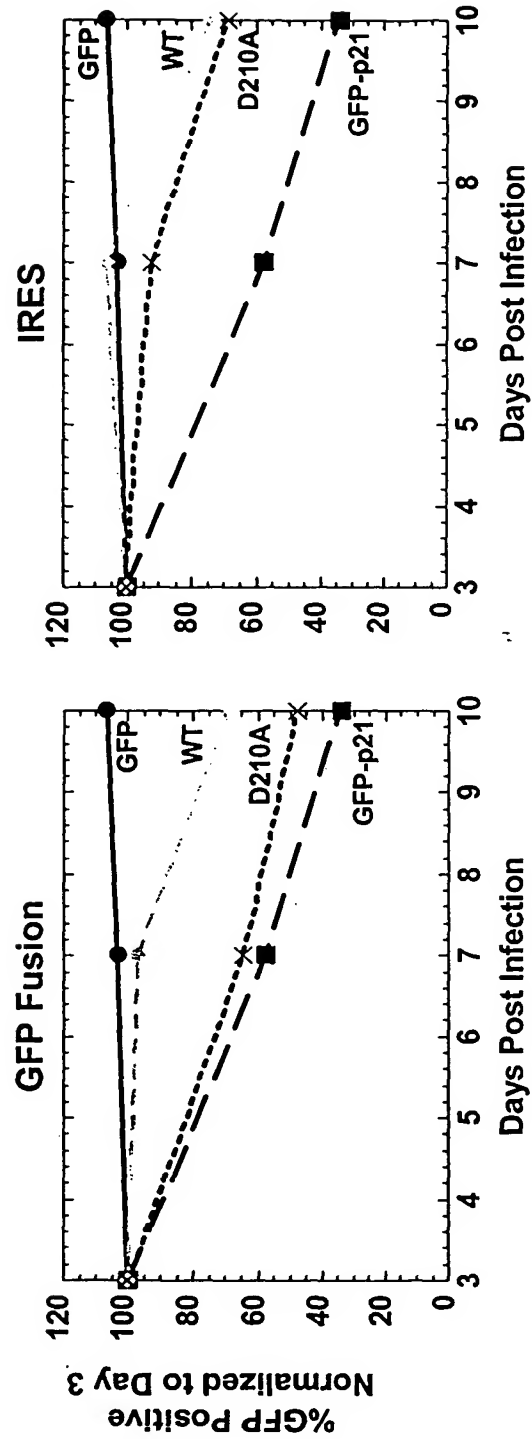


%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	49	49
GFP-p21	6.3	6.3
Ape1	8.2	7.1
Ape1 E96A	9.3	7.3
Ape1 D210A	8.4	4.9
Ape1 C65A	13.7	8.4

FIGURE 56

Both Ape1 WT and Ape1 D210A Are Antiproliferative in HMEC Cells

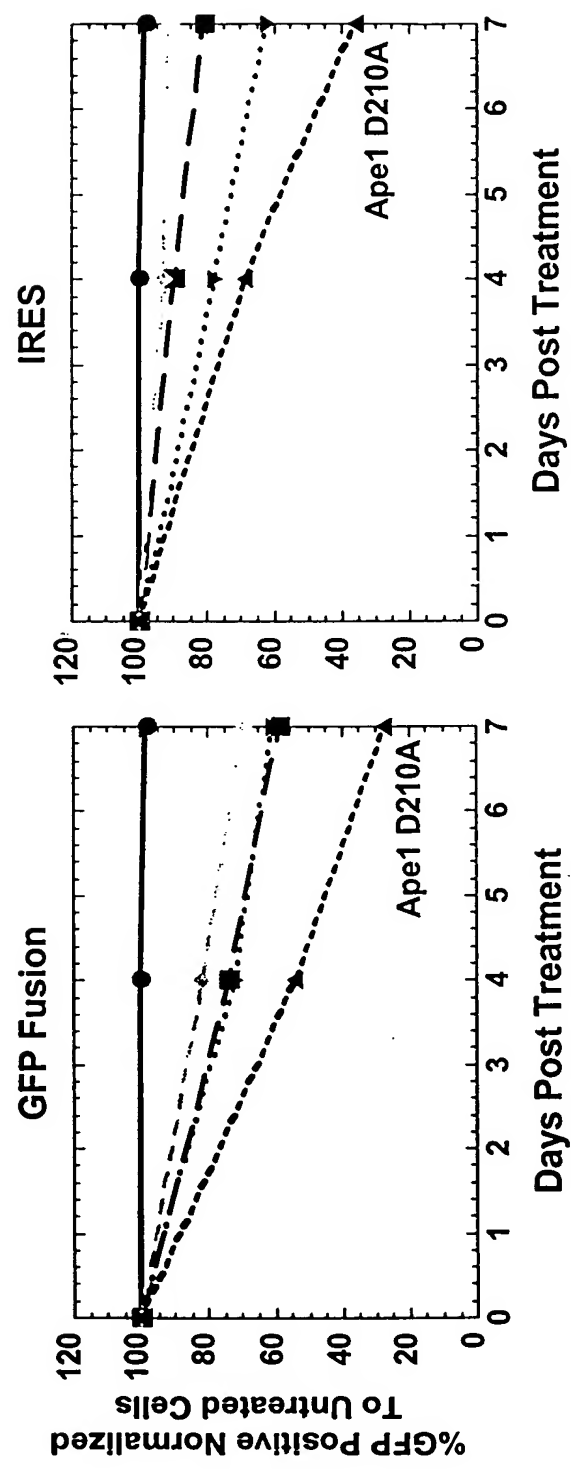


%GFP Positive (Day 3)

	GFP	IRES
GFP	30.7	30.7
GFP-p21	5.6	5.6
Ape1 WT	3.6	4.8
Ape1 D210A	5.2	4.2

FIGURE 57

Ape1 D210A Sensitizes A549 Cells to Methyl Methanesulfonate Treatment



At 72 hours after infection, A549 cells were treated with 3mM MMS for 60 min.

%GFP Positive at Day 3		
	GFP Fusion	IRES
○ — GFP	64.8	64.8
□ - Ape1	15.7	6.2
◇ · Ape1 E96A	17.2	9.9
· · · Ape1 D210A	11.3	6.1
· · · Ape1 C65A	16.8	3.3

FIGURE 58

Ape1 WT and C65A Are Protective in A549 Cells Treated with Bleomycin

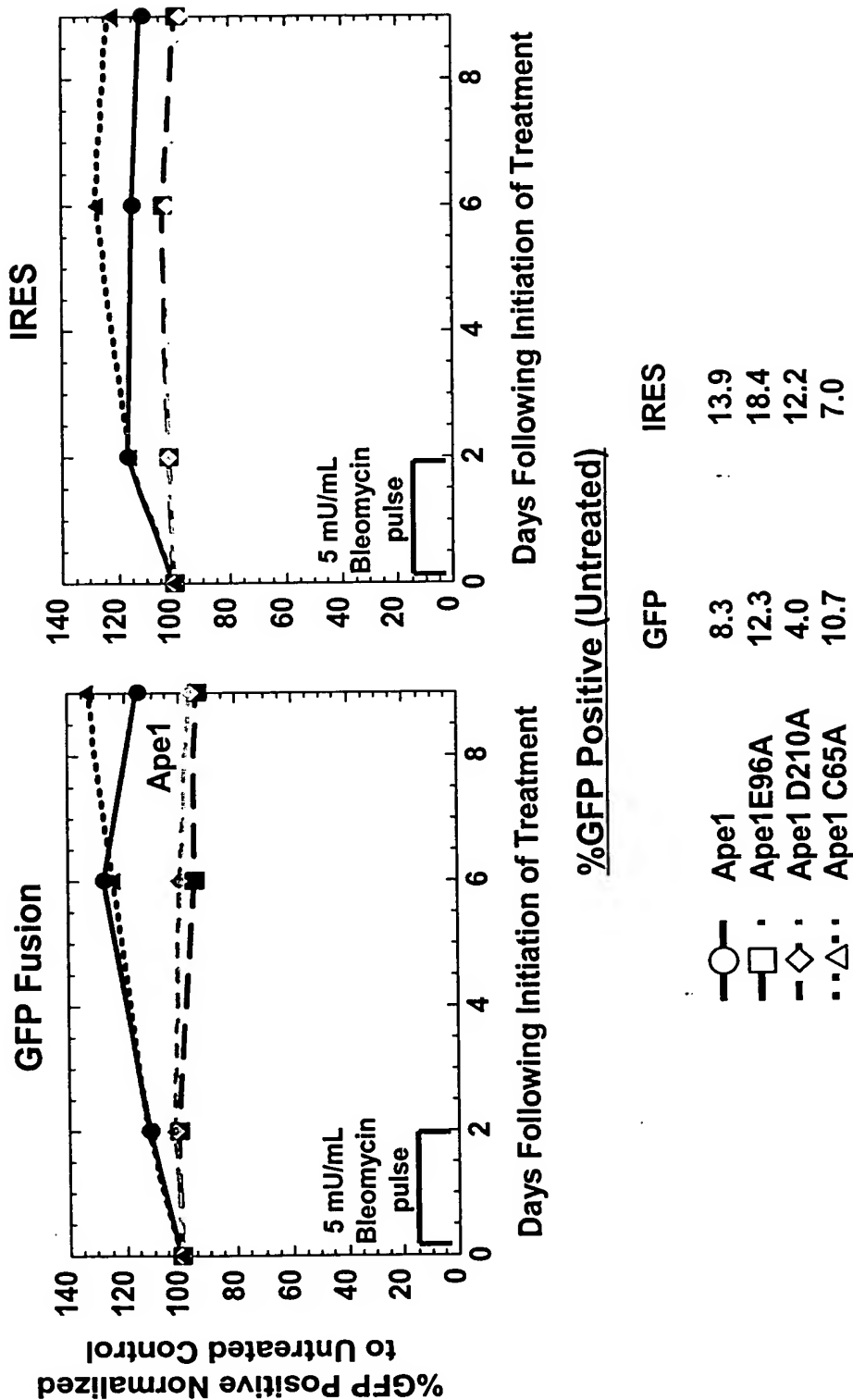


FIGURE 59

These results are consistent with those published by Robertson et al., *Cancer Res.* 2001 showing that overexpression of Ape1 in the tumor line NT2 confers resistance to bleomycin treatment.

Ape1 WT and C65A Are Protective in HeLa and H1299 Cells Treated with Bleomycin

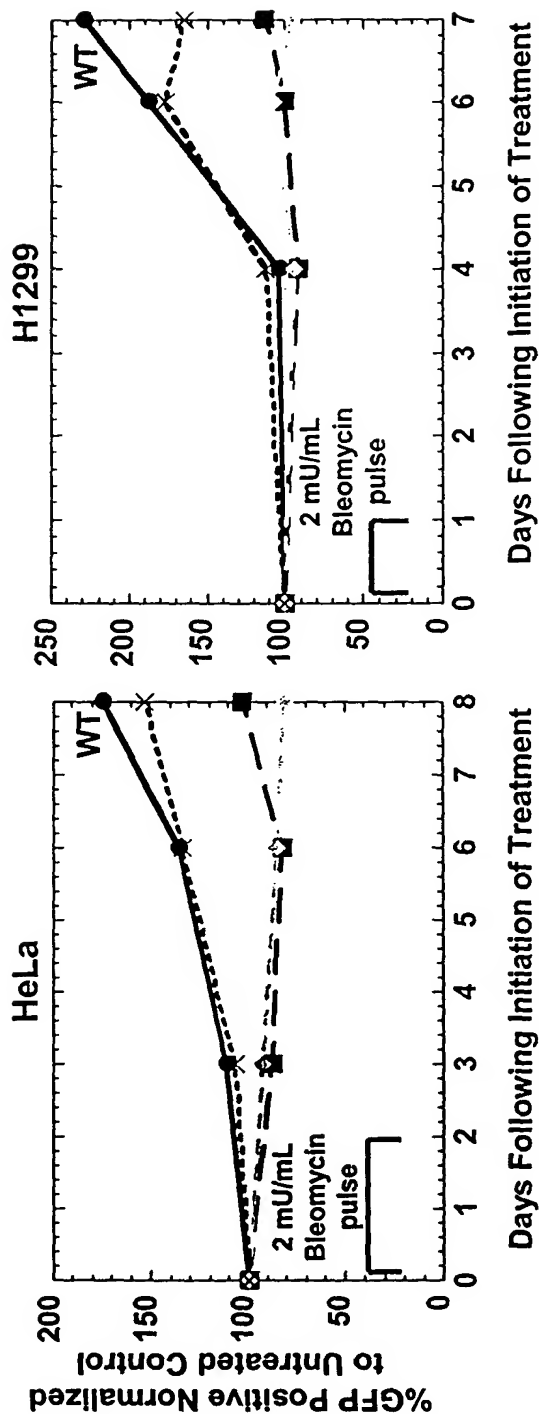


FIGURE 60

%GFP Positive (Untreated)

	HeLa	H1299
Ape1 WT	11.4	2.8
Ape1 E96A	12.4	5.2
Ape1 D210A	36.3	3.6
Ape1 C65A	36.1	3.6

IRES-Ape1 constructs were used for these experiments.

Tagman Analysis of CK2a Expression
Using RNA from Tumor Cell Lines

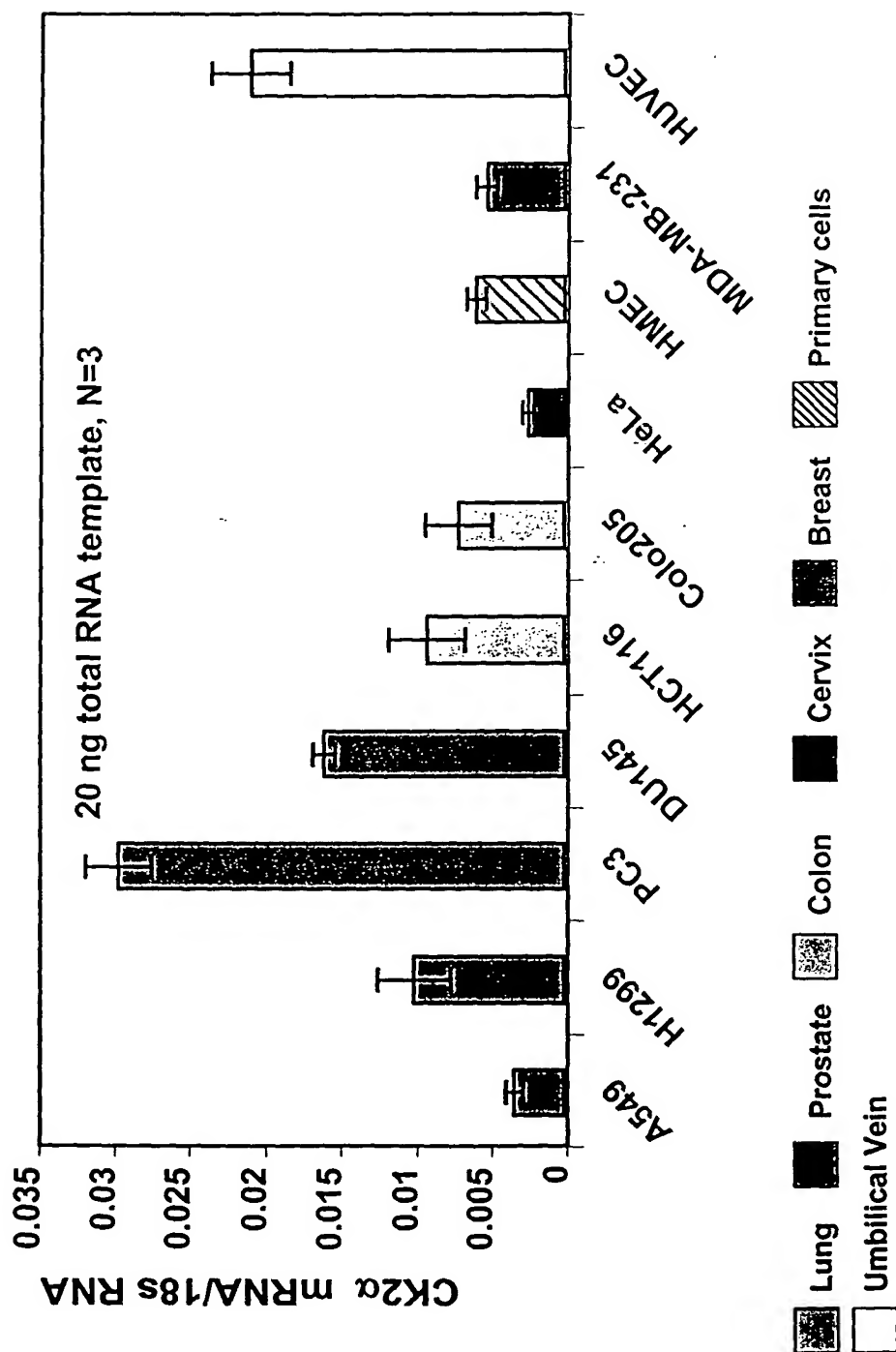


FIGURE 61

Dominant Negative Mutants for CK2α

Point mutants : K68A,D175N- K68A corresponds to a mutation considered essential for the phototransfer reaction in the kinase domain (Oncogene. 2001 Apr 12;20(16):2010-22. PMID: 11360185), D175N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

```

*->yelleklGeGsfGkVykakhkdkgtgiVavKilkkkesikekrflr
  Y+l++klG+G +++V++a+++ ++++V+vKilk ++k+ + r
CK2alpha 39 YQLVRKLGRGKYSEVFEAINI-TNNEKVVVKILK--PVKKKK--IKR 80

  EiqilkrLs.HpNIvrligvfed.tddhlylvmEymegGdLfdyllrrngg
  Ei+il +L+++ pNI++l +++ d+ ++ + lv+E+++++d +++ + +
CK2alpha 81 EIKILENLRGPNIIITLADIVKDPVSRTPALVFEHVNTDFKQLYQTLT- 129

  plsekeakkialQilrGleYlHsngivHRDLKpeNILLdendgtvKiaDF
  + +++++++il++l+Y+Hs+gi+HRD+Kp N+++++++ +++++D+
CK2alpha 130 ---DYDIRFYMYEILKALDYCHSMGIMHRDVKPHNVMDHEHRKRLIDW 176

  GLArlllesssklttfvGtpwYmmAPEvileg.rgysskvDvWSlGvilyE
  GLA ++++++ ++ +v ++++ PE+ l + ++Y+ D+WSlG++L+
CK2alpha 177 GLAEFYHPGQYNNVRVASRYFK-GPEL-LVDYQMYDYSLDMWSLGCMLAS 224

  lltggplfpgadlpafgtg.gd.evdqli.if.vlklpfsdelpktridpl
  + ++++++f+ ++++++ ++++++ ++ +++++ +d++++k++i+
CK2alpha 225 MIFRKEPFF-----HghDnYDQLVRIAKVLGTEDLYDYIDKYNIELD 266

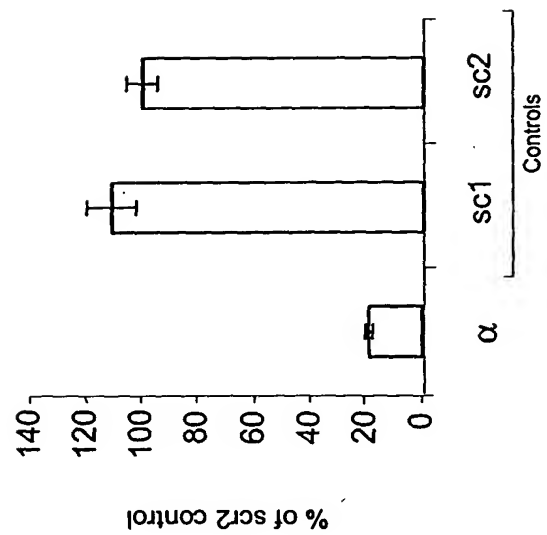
  eelfriiikrp.....glrlplpsncSeelkdLlkkcLnkDPskRpGsa
  + +i+ r+++++ +++ +++++++S+e++d+l+k+L+++D ++R+
CK2alpha 267 PRFNDILGRHsrkrwerFVHSENQHLVSPEALDFLDKLLRYDQSRLL--- 313

  takeilnhpwf<-*
  ta+e+++hp+f
CK2alpha 314 TAREAMEHPYF 324 Bold= the catalytic residues

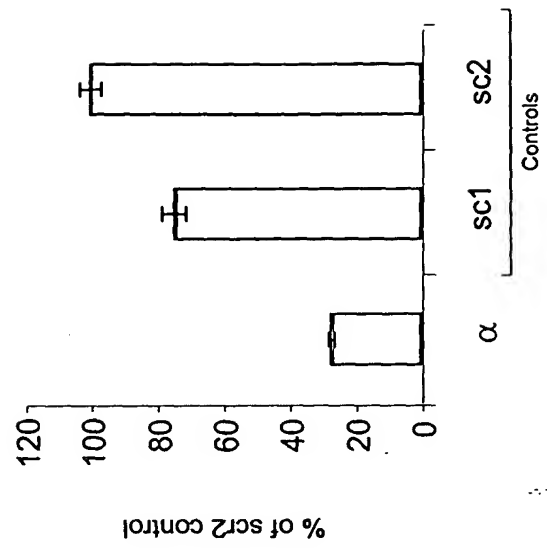
```

FIGURE 62

CK2 α -Specific siRNA is Antiproliferative in H1299 Cells



CK2 α mRNA level in H1299 after siRNA treatment (Taqman)



BrdU incorporation by H1299 treated with CK2 α siRNA

FIGURE 63

Sc1 and sc2 refer to scrambled siRNA controls

Tagman Analysis of KNIAMRE Expression
Using RNA from Tumor Cell Lines

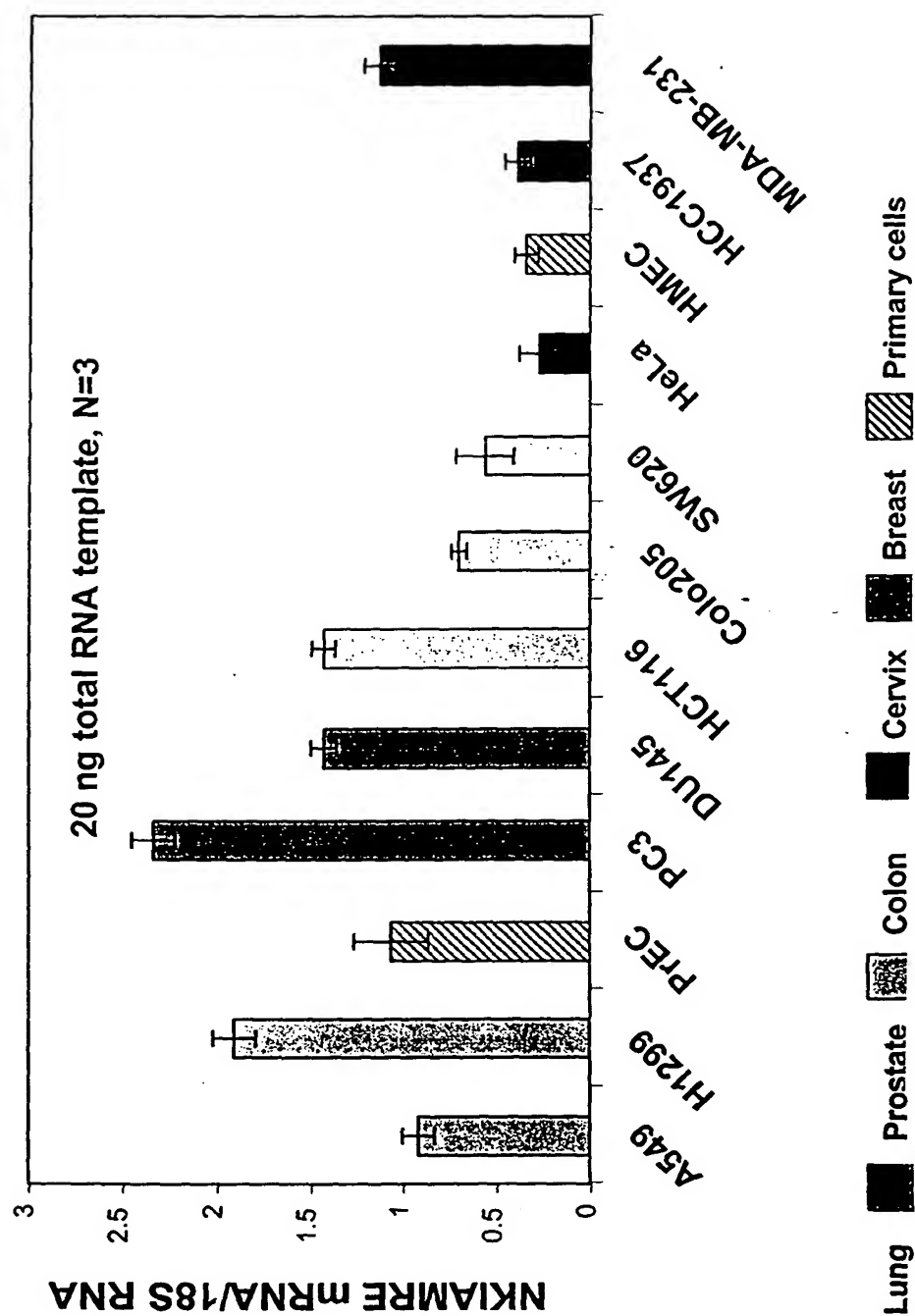


FIGURE 64

Dominant Negative Mutants for NKIAMRE

NKIAMRE active site mutants K33A, D143A

CDK2	MENFQKVEKIGEGTYGVVYKARNKLTGEVVVALKKIRLDTETEGVPSTAIRESLLKELNH		
NKIAMRE	MEMYETLGKVGEGSYGTMKCKHKNTGQIVAIKIFERPEQS-VNKIAMREIKFLKQFHH		
	** : : : * : : : * : : : * : : : * : : : * : : : *		
CDK2	PNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHS		
NKIAMRE	ENLVNLIIEVFRQKKIHLVFEFIDHTVLDELQHYCHG-LESKRRLRKYLFQILRAIDYLS		
	* : * : * : * : * : * : * : * : * : * : * : * : *		
CDK2	HRVLHRDLKPQNLLINTEGAIKLADFGLARAFGVPRVRYTHEVVTLYWYRAPEILLGCKYY		
NKIAMRE	NNI IHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYDYVATRWYRAPELVLKDTSY		
	: : : * : : * : : * : : : * : : : * : : : * : : : *		
CDK2	STAVDIWSLGCIFAEMVTRRALFPDSEIDQLFRIFRTLGTDPDEVVWPGVTSMPDYK-PS		
NKIAMRE	GKPVDIWALGCMIIEMATGNPYLPSSDDLHLHKIVLVKGNLSPHLQNI FSKSPIFAGVV		
	... * : : * : : * : : * : : * : : * : : * : : *		
CDK2	FPKWAR-QDFSKVPPPLEDEGRSLLSQMLHYDPNKRISAKAALAHFFQD--VTKPVPH		
NKIAMRE	LPQVQHPKNARKKYPKLNGLLADIVHACLIQIDPADRISSDDLHHHEYFTRDGFIEKFMPE		
	: * : : * : * : : : * : * : * : * : * : * : *		
CDK2	LRL-----		
NKIAMRE	LKAKLLQEAKVNSLIKPKESSKENELRKDERKTVYTNLTLLSSSVLGEIEKEKPKPKIKV		
	* : -----		
CDK2	RVIKVKGGRGDISEPKKKEYEGLGQQDANENVHPMSPDTKLVTIEPPNPINPSTNCNGL		
NKIAMRE	-----		
CDK2	KENPHCGGSVTMPPIINLTNSNLMAANLSSNLFHPSVR		
NKIAMRE	-----		

Mutation site

○ Mutation site

FIGURE 65

Dominant Negative Mutants for FEN1

FEN1 active site mutant D86A and D181A (PMID: 8621570, 10409728)

XPG_N domain*	->MGIkGLlpiLkpvapeairsvsIEalegYYkvLAiDasiwLyqfLka	
FEN1	1	MGI+GL+++++vap+air++++i++++g +++AiDas++++yqfL+a MGIQGLAKLIADVAPSAIRENDIKSYFG--RKVAIDASMSIYQFLIA 45
XPG_N domain		vRdqlgnnlenEeGettshlmglfSRlcrLldfgikPifVFDGgapndkK
FEN1	46	vR q g+ l+nEeGettshlmg+f+R+r++++gIkP++VFDG++p +lK VR-QGGDVLQNEEGETTSHLMGMFYRTIRMENGIKPVYVFDGKPP-QLK 93
XPG_N domain		aetlqKRsarrqea<-*
FEN1	94	+++l+KRs+rr+ea SGELAKRSERRAEA 107
XPG_I domain*	->rlmGIpyIvAPgVEAEAQcayLekkglvdgiiteDsDvLLFGaprll	
FEN1	146	+lmGIpy +AP+ EAEA ca+L+k+g+v++++TeD+D+L FG+p+l+ SLMGIPYLDAPS-EAEASCAALVKAGKVAAATEDMDCLTFGSPVLM 191
XPG_I domain		rnLtlsgkksgPsitslkveieeidlesllrelgigklsregLidlailL
FEN1	192	r+Lt s++k k++i+e++l++++l+elgL ++eq++dl+iLl RHLTASEAK-----KLPIQEFHLSRILQELGL---NQEQFVLDLCILL 230
XPG_I domain		GcDYteG<-*
FEN1	231	G+DY+e+ GSDYCES 237
		○ Mutation site

FIGURE 66

Expression of FEN1 Dominant Negative Mutants in A549 Cells is Antiproliferative

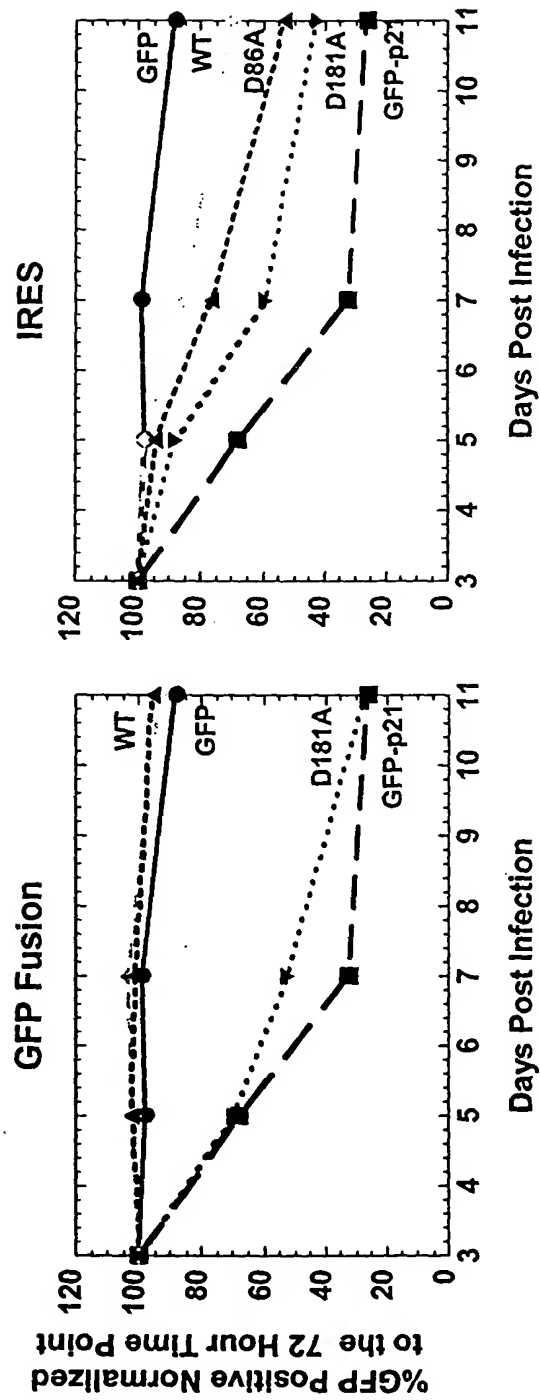


FIGURE 67

Expression of FEN1 Dominant Negative Mutants is Antiproliferative in H1299 Cells

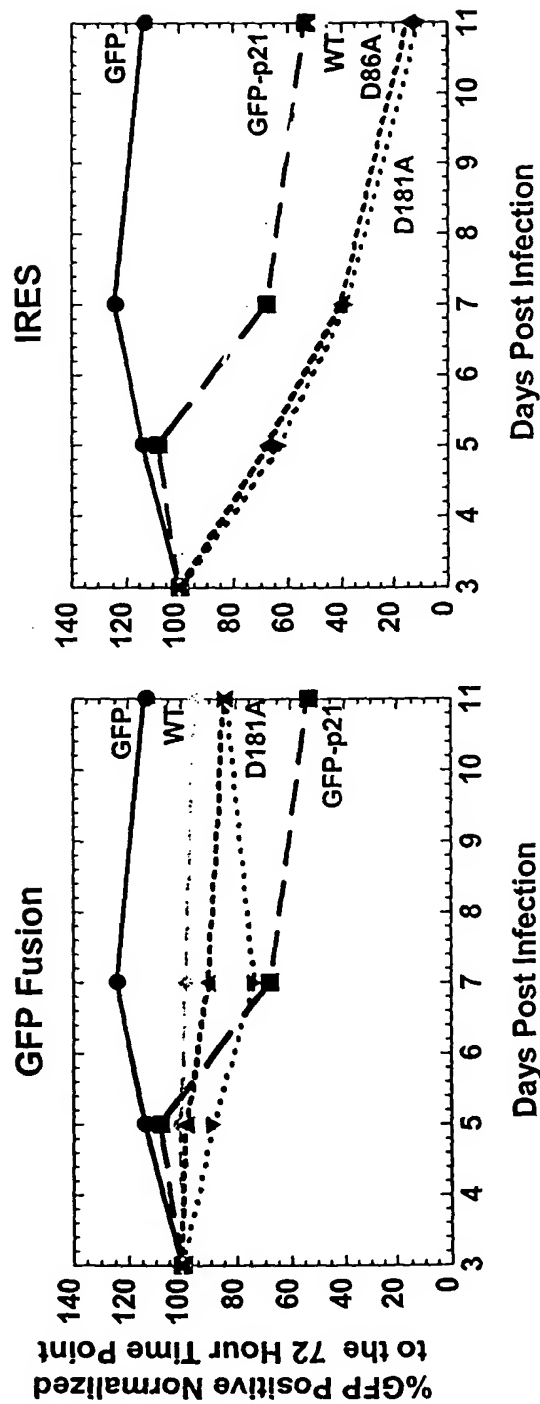


FIGURE 68

%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	58.1	58.1
GFP-p21	3.9	3.9
Fen1 WT	34.4	25.9
Fen1 D86A	34.1	58.0
Fen1 D181A	48.3	59.7

CDK3 active site mutants K33A, D145A

FIGURE 69

Expression of CDK3 Dominant Negative Mutants Has No Antiproliferative Effect in A549 Cells

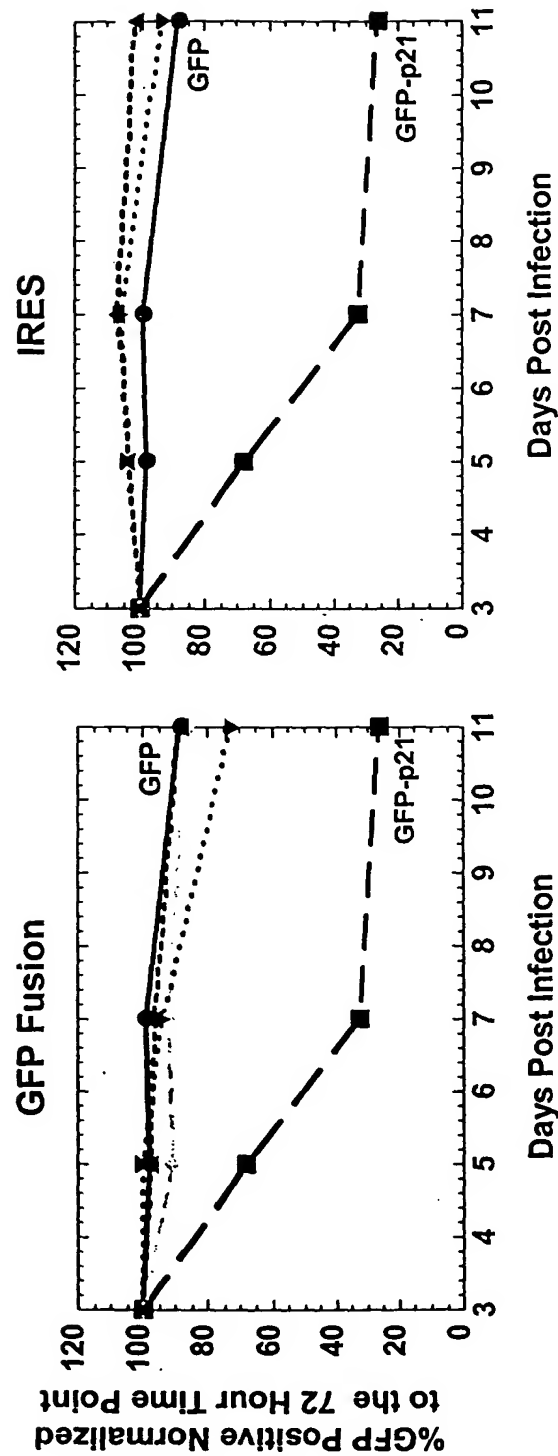


FIGURE 70

%GFP Positive at 72 Hours	
GFP Fusion	IRES
GFP	85.3
GFP-p21	19.5
CDK3 WT	57.2
CDK3 K33A	57.7
CDK3 D145A	51.5

Expression of CDK3 Dominant Negative Negative Mutants Has No Antiproliferative Effect in H1299 Cells

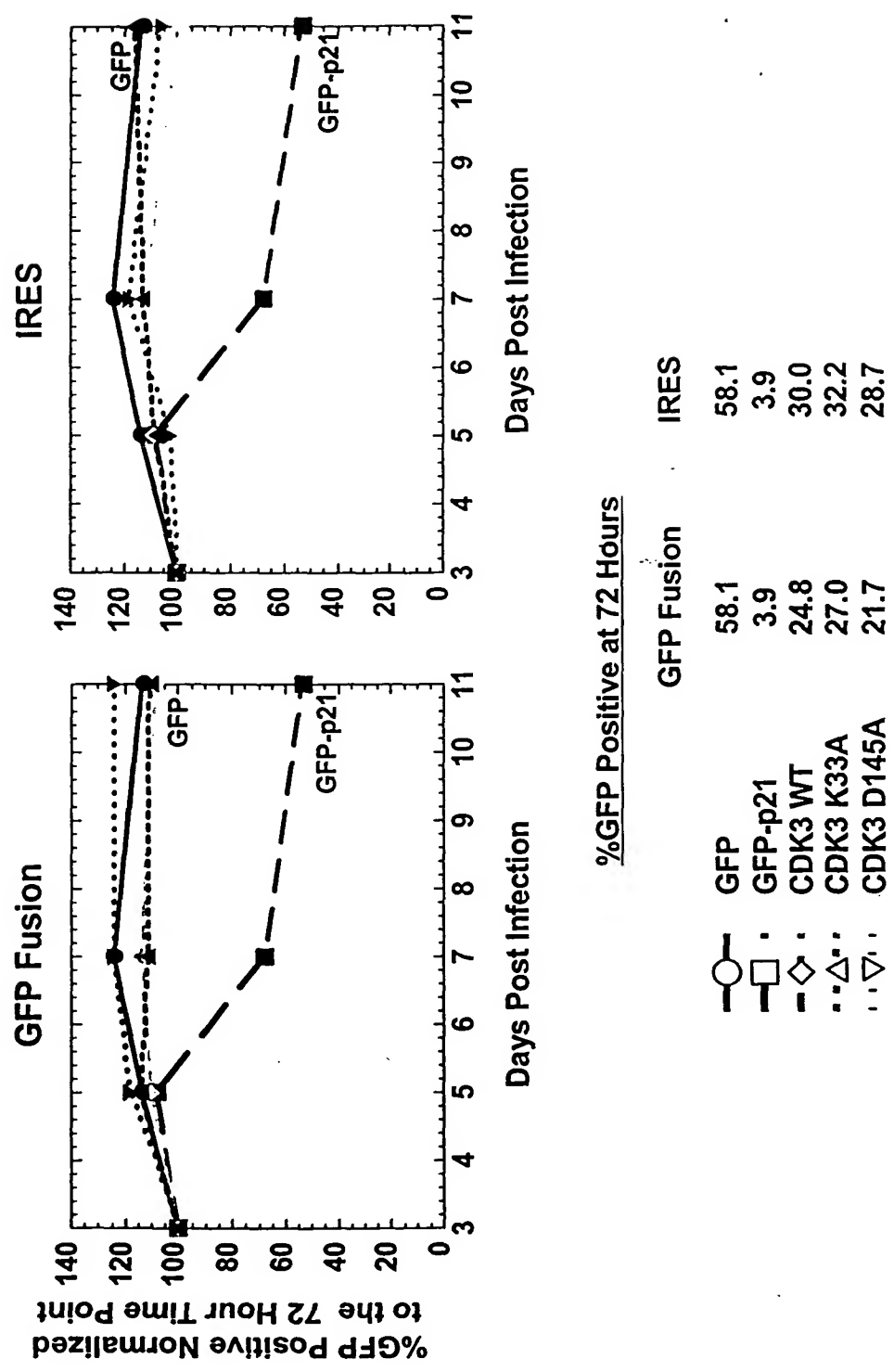


FIGURE 71

Dominant Negative Mutants for HBO1

HBO1 active site mutants, G485E, L497S, E508Q, The G315 mutant, the L327S mutant and the E338Q mutant in yEsa1 abolished the catalytic activity (PNAS, p3561, 1998, MCB, p2515, 1999, Mol.Cell, p1195, 2000). G315 is involved in CoA binding (Mol.Cell, p1195, 2000).

HBO1 YHSPYPEYARLGRLYMCEFCCLKYMKSQTLRRHMAKCVWKHPGDEIYRKGSISVFEVD
yEsa1 YFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKCKTLRHPPGNEIYRDDYVSFFEID
..*.*.* : . :.* : * :.* : * :. :.* : * :. :.* : * :. :.* : * :. :.* : *

HBO1 GKKNKIYQNLCLLAKFLDHKTLYYDVEPFLFYVMTADNTGCHLIGYFSKEKNSFLNY
yEsa1 GRKQRTWCRNLCLLSKFLDHLKTLTYDVPFLFYCMTRRDELGHHLVGYFSKEKESADGY
..*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *

HBO1 NVSCILTMPQYMRQGYGKMLIDFSYLLSKVEKVGSPERPLSDGLISRSYWKEVLLRY
yEsa1 NVACILTLQPQYQRMGYGKLLIEFSYELSKKENKVGSPKPLSDGLLSYRAYWSDTLITL
315 327 338
..*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *

HBO1 LHNFGKEISIKESQETAVNPVDIVSTLQALQMLKYWKGHVLVKRQDLIDEWIAKEAK
yEsa1 LVEHQ-KEITIDEISSMTSMTTDLHTAKTLNLRKYKGQHIIFLNEDILDYRNRLKAK
..*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *.*.*.*.* : *

HBO1 RSNSNKTMDPCLKWTPPKGT-----
yEsa1 K---RRTIDPNRLIWKPPVFTASQLRFAW
: . :.*.*.*.* : *.*.*.*.* : *

○ Mutation site

FIGURE 72

Dominant Negative Mutants for PIM-1

Point mutant : K67A, D186N - D186N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

```

*->yelleklGeGsfGkVykakhkdkgtkiVAVKilkkekesikek....
      y+++ lG+G+fG+Vy +++++ +++ +VA+K + k ++++++ +
PIM1 38 YQVGPLLGGGFGSVYSGIRV-SDNLPVAIKHVE--KDRISDWgelp 81

      rflrEiqilkrLs..HpNIvrligvfedtdhlylvmEymegG.dLf
      +++r+ +E+ +lk+++s++ +rll+++fe ++d++ l++E e +dLf
PIM1 82 ngrVPMEVVLLKKVSSGFGVIRLLDWE-RPDSFVLILERPEPVqDLF 130

      dylrrnggplsekeakkialQilrGleYlHsngivHRDLKpeNILldend
      d+++++g +l e+ a+++++Q+l+++ ++H++g++HRD+K eNIL+d n+
PIM1 131 DFITERG-ALQEEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNR 179

      gtvKiaDFGLArlllessklttfvGTpwYmmAPEvileg.rgysskvDvW
      g +K++DFG +ll+ ++ +t+f GT++Y +PE+ +++++r+++ + vW
PIM1 180 GELKLIDFGSGALLK-DTVYTFDGTGRVYS-PPew-IRYhRYHGRSAAvW 226

      SlGvilyElltgglfpfgadlpafggdevdqliifvklpfdselpktr
      SlG++Ly +++g
PIM1 227 SLGILLYDMVCG-----DIPFEH----- 244

      idpleelfriikrpglrlplpsncseelkdLlkkLnkDPskRpGsatak
      ee+ r++ + +++S+e+++L+++CL++ Ps+Rp t++
PIM1 245 ---DEEIIIRGQVF-----FRQRVSSECQHLIRWCLALRPDRP---TFE 282

      eilnhpwf<-*
      ei nhpw+
PIM1 283 EIQNHPWM 290

```

○ Mutation site

FIGURE 73

No Significant Antiproliferative Effect is Observed With GFP-NKIAMRE Dominant Negative Mutants in Either A549 or H1299 Cells

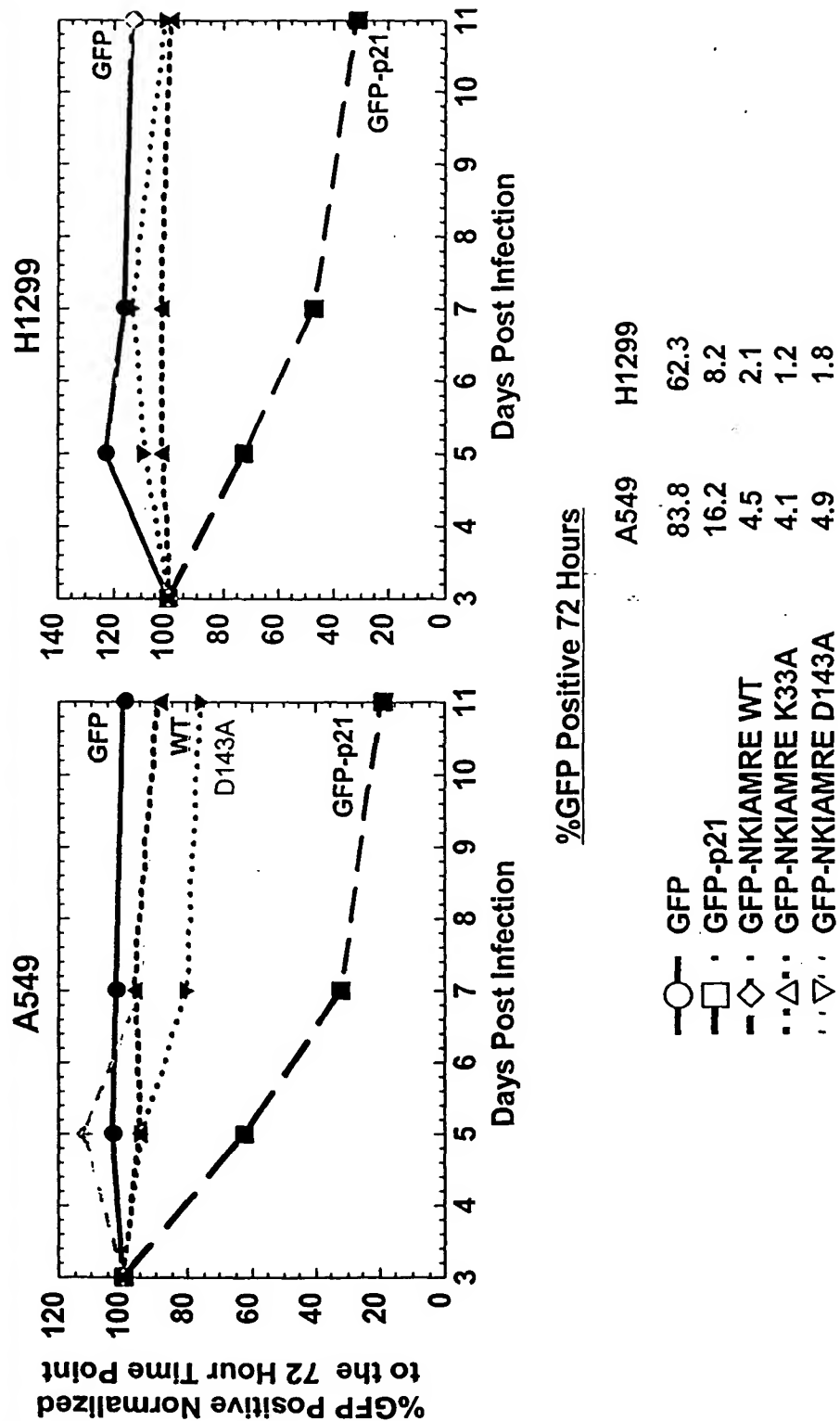


FIGURE 74